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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:16:31 ; Search time 38 Seconds  
(without alignments)  
1570.955 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 448  
Sequence: 1 MSQSTQTFNEFLSPVFOHIM.....PKQSDVFRHRSKPNRSYYP 448

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A\_Geneseq\_101002.\*

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	448	20	AAV45246 Human p51 protein
2	448	100.0	448	20	AAV05955 Human cell regulat
3	448	100.0	448	21	AAAB11359 Human p63 protein
4	448	100.0	448	22	AAAB2128 Human protein #1 u
5	448	100.0	448	23	AAAB74991 Human p53 homologu
6	410	91.5	516	20	AAV05954 Human cell regulat
7	410	91.5	516	21	AAAB11363 Human p63 protein
8	410	91.5	516	23	AAAB74995 Human p53 homologu
9	410	91.5	641	20	AAV45247 Human p51 protein
10	410	91.5	641	20	AAV05953 Human cell regulat

11	410	91.5	641	21	AAAB11358 Human p63 protein
12	410	91.5	641	22	AAAB2129 Human protein #2 u
13	410	91.5	641	23	AAAB74990 Human p53 homologu
14	410	91.5	680	21	AAAB11361 Human p63 protein
15	410	91.5	680	21	AAV50997 Human K57 protein
16	410	91.5	680	23	AAAB74993 Human p53 homologu
17	379	84.6	393	20	AAV05957 Human cell regulat
18	341	76.1	461	21	AAAB11362 Human p63 protein
19	341	76.1	461	23	AAAB74994 Human p53 homologu
20	341	76.1	586	20	AAV05956 Human cell regulat
21	284	63.4	483	20	AAV05958 Human cell regulat
22	284	63.4	680	20	AAV05958 Human cell regulat
23	272	60.7	586	21	AAAB11357 Human p63 protein
24	272	60.7	586	23	AAAB74989 Human p53 homologu
25	269	60.0	356	20	AAV43135 Human p40 protein
26	269	60.0	356	21	AAAB11360 Human p63 protein
27	269	60.0	356	23	AAAB74992 Human p53 homologu
28	259	57.8	389	20	AAV05964 Mouse cell regulat
29	259	57.8	461	20	AAV05963 Mouse cell regulat
30	259	57.8	586	20	AAV05962 Rat KET protein
31	248	55.4	680	21	AAV50998 Human lung tumor a
32	191	42.6	586	20	AAV41032 Human lung cancer
33	191	42.6	586	21	AAAB11317 Human lung tumor
34	191	42.6	586	23	AAAB74949 Mouse cell regulat
35	49	10.9	155	20	AAV05960 p73 gamma protein
36	49	10.9	403	22	AAAB84840 p73 gamma protein
37	22	4.9	475	22	AAAB84839 Human p53 tumor s
38	22	4.9	499	18	AAW36190 Monkey p53 tumor s
39	22	4.9	499	21	AAV44635 Human p73 beta spl
40	22	4.9	499	21	AAV44635 Human p73 beta spl
41	22	4.9	499	22	AAAB84838 Human p53 tumor s
42	22	4.9	506	18	AAW36188 Human p53 tumor s
43	22	4.9	587	18	AAW36187 Human p53 tumor s
44	22	4.9	588	18	AAW36189 Human p53 tumor s
45	22	4.9	635	20	AAW30661 Human NBS-1 alpha

#### ALIGNMENTS

RESULT 1	
AAV45246	standard; Protein; 448 AA.
AAV45246	
AC	AAV45246;
AC	
DT	07-JAN-2000 (first entry)
DT	
DE	Human p51 protein A.
DE	
XX	
XX	Human; p51; p53 related gene; cell proliferation; regulation; cancer;
KW	tumour suppression; diagnosis.
KW	
OS	Homo sapiens.
OS	
FT	Key
FT	Domain
FT	Location/Qualifiers
FT	1..39
FT	/label= transactivation_domain
FT	142..321
FT	/label= DNA_binding_domain
FT	353..397
FT	/label= oligomerisation_domain
FT	
PN	W09950412-A1.
PN	
XX	
XX	07-OCT-1999.
PD	
XX	
XX	
XX	24-MAR-1999; 99WO-JP01512.
PP	
XX	
PR	27-MAR-1998; 98JP-0100467.
XX	
XX	
PA	(SAKA ) OTSUKA PHARM CO LTD.
PA	(IKAWA ) IKAWA Y.

XX Ikawa Y, Ikawa S, Obinata M;  
XX  
XX WPI: 1999-591318/50.  
DR N-PSDB; AAZ25770.  
XX

XX New p53 related human gene p51, useful for diagnosis, investigation and  
XX treatment of cancers and screening for potential cell proliferation  
XX agents -

PS Claim 1; Page 147-148; 163pp; Japanese.

CC The present sequence represents a human p51 protein, which is related to  
CC p53 and has cell proliferation regulation and tumour suppression  
CC activity. The p51 gene can be used in the investigation, diagnosis and  
CC treatment of diseases such as cancer, with which the p53 family cell  
CC proliferation regulation is associated. The p51 protein may be used for  
CC screening potential agonists and antagonists of its regulatory function,  
CC for use as drugs,  
XX

SO Sequence 448 AA;

Query Match 100.0%; Score 448; DB 20; Length 448;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPFVFOHIMDFLEOPICSVOPIDLNFEVDESEGDATNKRIETSMDCIRMO 60  
DB 1 MSOSTOTNEFLSPFVFOHIMDFLEOPICSVOPIDLNFEVDESEGDATNKRIETSMDCIRMO 60  
QY 61 DSLSLDPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFDAL 120  
DB 61 DSLSLDPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFDAL 120  
QY 121 SPSPAIPSNTRYDGPSPFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180  
DB 121 SPSPAIPSNTRYDGPSPFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180  
QY 121 SPSPAIPSNTRYDGPSPFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180  
DB 121 SPSPAIPSNTRYDGPSPFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180  
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVDP 240  
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVDP 240  
QY 241 ITGROSIVLYPEPQVGTETFTVLYNMCNCSGCGVGNRRPILITVLETRDGOVIGRRC 300  
DB 241 ITGROSIVLYPEPQVGTETFTVLYNMCNCSGCGVGNRRPILITVLETRDGOVIGRRC 300  
QY 301 FEARICACPGDRKADSDIRKQOVSDSTKNGDGTKRPFRONTNGIOMTSIKRRSPDDE 360  
DB 301 FEARICACPGDRKADSDIRKQOVSDSTKNGDGTKRPFRONTNGIOMTSIKRRSPDDE 360  
QY 361 LLYIYPVGRGTYEMLKIKESLELMQYLPQHTIETRYRQOQOQHILQKHLISACFRNE 420  
DB 361 LLYIYPVGRGTYEMLKIKESLELMQYLPQHTIETRYRQOQOQHILQKHLISACFRNE 420  
QY 421 LVEPRRETPKOSQVFFPHSKPPNRSYYP 448  
DB 421 LVEPRRETPKOSQVFFPHSKPPNRSYYP 448

RESULT 2

AAI05955

ID AAY05955 standard; Protein; 448 AA.

AC AAY05955;

DT 16-AUG-1999 (first entry)

DE Human cell regulatory protein p63, isoform hUTAP63 gamma.

KW Cell regulatory protein; p63; hUTAP63 gamma; Tap63 gamma; human;

KW cancer; tumour suppressor; cell cycle control; apoptosis;

KW cell proliferation; cell differentiation; therapy.

OS Homo sapiens.

PN WO9919357-A2.

PD 22-APR-1999.

PF 02-OCT-1998; 98WO-US21992.

PR 29-MAY-1998; 98US-0087216.

PR 15-OCT-1997; 97US-0062076.

XX (HARD) HARVARD COLLEGE.

XX McKeon F, Yang A;

XX WPI: 1999-277595/23.

DR N-PSDB; AAX58574.

XX New isolated p63 cell regulatory protein for, e.g. treatment of  
XX tumours

PS Claim 23; Fig 11; 161pp; English.

CC The present invention concerns the discovery of a new family of  
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
CC which demonstrate certain sequence identity to known tumour  
CC suppressor proteins p53 and p73. It has been observed that the  
CC known exon and intron sizes for these 2 genes, it was possible to  
CC identify new members of this gene family using a PCR-based strategy  
CC of amplifying 2 exons in a conserved domain and their intervening  
CC intron. The human p53 gene was localised to chromosomal position  
CC 3q27-29. At least 6 different isoforms exist. Splice variants  
CC differing at the C-terminus have been designated as alpha, beta and  
CC gamma forms, while p53 members differing in the N-terminus are  
CC designated as delta and TA forms, where the delta form lacks the  
CC transactivation domain. The present sequence represents human  
CC p63 isoform p63 gamma. p63 was detected in a variety of  
CC human and mouse tissue. It demonstrates remarkably divergent  
CC activities, such as the ability to transactivate p53 reporter genes  
CC and induce apoptosis. Cessation or down-regulation of p63 expression  
CC may play a critical role in the process of cervical squamous  
CC differentiation, both benign and neoplastic. Delta isoforms of p63  
CC act as dominant negatives towards transactivation by p53 and p63.  
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
CC cachexia) and neuronal differentiation and related degenerative  
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see  
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to  
CC identify compounds useful for treating disorders involving such  
CC processes, in detection and diagnosis, and in the production of  
CC transgenic animals.

SO Sequence 448 AA;

Query Match 100.0%; Score 448; DB 20; Length 448;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPFVFOHIMDFLEOPICSVOPIDLNFEVDESEGDATNKRIETSMDCIRMO 60  
DB 1 MSOSTOTNEFLSPFVFOHIMDFLEOPICSVOPIDLNFEVDESEGDATNKRIETSMDCIRMO 60  
QY 61 DSLSLDPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFDAL 120  
DB 61 DSLSLDPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFDAL 120  
QY 121 SPSPAIPSNTRYDGPSPFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180  
DB 121 SPSPAIPSNTRYDGPSPFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180  
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVDP 240  
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVDP 240

QY	241	ITRQSGVILVPEPPQVGTETFTVILNFMCNSSCVGAMRRPILIVLTETRDGQVLRRC	3000
Db	241	ITRQSGVILVPEPPQVGTETFTVILNFMCNSSCVGAMRRPILIVLTETRDGQVLRRC	3000
QY	301	FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRPFRRONTGIGIOMTSIKRRSPDE	3600
Db	301	FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRPFRRONTGIGIOMTSIKRRSPDE	3600
QY	361	LVLPLPRGKETTEMLIKTESLEMQYLPOFTIETFRQOQOQHOLQKHLISACRNE	4200
Db	361	LVLPLPRGKETTEMLIKTESLEMQYLPOFTIETFRQOQOQHOLQKHLISACRNE	4200
QY	421	LVEPRRETPKQSDVFFRRHSKPPNRSVYP	448
Db	421	LVEPRRETPKQSDVFFRRHSKPPNRSVYP	448
RESULT 3			
AA	1359	AAAB1359 standard; Protein; 448 AA.	
AC	AAAB1359;		
DT	21-FEB-2001 (first entry)		
DE	Human p63 protein isoform #3.		
KX	Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;		
KW	vaccine; detection.		
OS	Homo sapiens.		
PN	WO200061612-A2.		
XX	19-OCT-2000.		
XX	03-APR-2000; 2000MO-US08896.		
XX	02-APR-1999; 99US-0285479.		
PR	17-DEC-1999; 99US-0466396.		
PR	30-DEC-1999; 99US-0476496.		
PR	10-JAN-2000; 2000US-0480884.		
PR	22-FEB-2000; 2000US-0510376.		
PA	(CORI-) CORIXA CORP.		
PI	Wang T, Fan L;		
DR	WPI; 2000-628399/60.		
DR	N-PSDB; AAC66029.		
PT	Isolated polypeptide comprising an immunogenic portion of a lung tumor		
PT	protein is used for detecting and monitoring progression of lung cancer		
PT	in a patient -		
PS	Disclosure; Page 247-249; 261pp; English.		
XX			
XX			
CC	This invention describes a novel isolated polypeptide (I) which		
CC	comprising an immunogenic portion of a lung tumor protein or variant (P2)		
CC	which have cytostatic activity. The polypeptides and polynucleotides are		
CC	used in compositions and vaccines to inhibit the development of cancer,		
CC	especially lung cancer, in a patient. Methods described in the invention		
CC	can be used to monitor the progression of a cancer by carrying out the		
CC	detection at subsequent time points and comparing the results from the		
CC	different time points. CD4+ and/or CD8+ T-cells isolated from a patient		
CC	are treated with P2, polynucleotides encoding P2 or antigen presenting		
CC	cells expressing P2 and then administered to the patient to inhibit		
CC	development of cancer.		
XX			
XX			
XX	Sequence 448 AA;		

Query Match 100.0%; Score 448; DB 21; Length 448;

[illegible]

PT of cancer, comprises a transcription activating region and a DNA  
binding region -

Example 1; Page 30-32; 57pp; Japanese.

CC The present invention relates to a chimera gene of p53 family encoding a  
CC transcription activating region, a DNA binding region, and an oligomer  
CC formation region of different p53 family proteins. The chimera gene can  
CC be used for gene therapy of p53 variant human tumours, and analysis of  
CC the function of the p53 family gene. The present sequence was used in the  
CC present invention.

XX Sequence 448 AA;

Query Match 100.0%; Score 448; DB 22; Length 448;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSOSTQTNTEFLSPFHOHIMDFLEOPICSVOPIDLNFDVDEPSEDEGATNKIEISMDCIKRMQ 60
QY 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
DB 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
QY 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTTP 180
DB 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTTP 180
QY 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSTRENEGOIAPPSHLIRVGENSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSTRENEGOIAPPSHLIRVGENSHAQYVEDP 240
QY 241 ITGQSVLYVPEPPQVTEFTTLYLYNFMCSNCSGVGMNRRPILITLTETRDGOVYGRRC 300
DB 241 ITGQSVLYVPEPPQVTEFTTLYLYNFMCSNCSGVGMNRRPILITLTETRDGOVYGRRC 300
QY 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTTRPRONTNHIOMTISIKRRSPDDE 360
DB 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTTRPRONTNHIOMTISIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKHLISACFENE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKHLISACFENE 420
QY 421 LVEPRRETPKOSDVFFRHSKPPNRSYYP 448
DB 421 LVEPRRETPKOSDVFFRHSKPPNRSYYP 448
```

RESULT 5  
ABBT4991  
ID ABBT4991 standard; Protein; 448 AA.

XX ABBT4991;

DT 01-MAY-2002 (first entry)

DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:340.

KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

XX Immune response.

OS Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.  
PR 21-AUG-2000; 2000US-0643597.  
PR 15-SEP-2000; 2000US-0662786.  
PR 09-OCT-2000; 2000US-0685696.  
PR 12-DEC-2000; 2000US-0735705.  
PR 07-MAY-2001; 2001US-0850716.

(CORI-) CORIXA CORP.

PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
PI McNeill PD, Fanger N, Reller MW, Marnerakis M, Fanger GR;  
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

DR WPI; 2002-090513/12.  
DR N-PSDB; ABL49248.

PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
lung cancer or stimulating an immune response -

XX Example 2; Page 322-323; 374pp; English.

CC The present invention describes human lung tumor proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. ABL4959 to ABL49300 and ABBT4946 to  
CC ABBT5070 represent sequences used in the exemplification of the present  
CC invention.

XX Sequence 448 AA;

Query Match 100.0%; Score 448; DB 23; Length 448;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSOSTQTNTEFLSPFHOHIMDFLEOPICSVOPIDLNFDVDEPSEDEGATNKIEISMDCIKRMQ 60
DB 1 MSOSTQTNTEFLSPFHOHIMDFLEOPICSVOPIDLNFDVDEPSEDEGATNKIEISMDCIKRMQ 60
QY 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
DB 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
QY 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTTP 180
DB 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTTP 180
QY 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSTRENEGOIAPPSHLIRVGENSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSTRENEGOIAPPSHLIRVGENSHAQYVEDP 240
QY 241 ITGQSVLYVPEPPQVTEFTTLYLYNFMCSNCSGVGMNRRPILITLTETRDGOVYGRRC 300
DB 241 ITGQSVLYVPEPPQVTEFTTLYLYNFMCSNCSGVGMNRRPILITLTETRDGOVYGRRC 300
QY 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTTRPRONTNHIOMTISIKRRSPDDE 360
DB 301 FEARICACPGDRKADSDSIRKQOVSDSTKNGDGTTRPRONTNHIOMTISIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKHLISACFENE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKHLISACFENE 420
QY 421 LVEPRRETPKOSDVFFRHSKPPNRSYYP 448
DB 421 LVEPRRETPKOSDVFFRHSKPPNRSYYP 448
```

RESULT 6  
AAAY05954  
ID AAAY05954 standard; Protein; 516 AA.



XX AAY05954;  
 AC 16-AUG-1999 (first entry)  
 XX  
 DE Human cell regulatory protein p63, isoform hUTAP63 beta.  
 XX  
 KW Cell regulatory protein: p63; hUTAP63 beta; TAP63 beta; human;  
 KW cancer; tumour suppressor; cell cycle control; apoptosis;  
 KW cell proliferation; cell differentiation; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M09919357-A2.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 02-OCT-1998; 98WO-US21992.  
 XX  
 PR 29-MAY-1998; 98US-0087216.  
 PR 15-OCT-1997; 97US-0062076.  
 XX  
 PA (HARD) HARVARD COLLEGE.  
 XX  
 PI McKeon F, Yang A;  
 XX  
 DR WPI: 1999-277595/23.  
 DR N-PSDB: AAY58573.  
 XX  
 PT New isolated p63 cell regulatory protein for, e.g. treatment of  
 PT tumours  
 XX  
 PS Claim 23; Fig 10; 161pp; English.  
 XX  
 CC The present invention concerns the discovery of a new family of  
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
 CC which demonstrate certain sequence identity to known tumour  
 CC suppressor proteins p53 and p73. It has been observed that the  
 CC intron-exon organisation is conserved between p73 and p53, and from  
 CC known exon and intron sizes for these 2 genes, it was possible to  
 CC identify new members of this gene family using a PCR-based strategy  
 CC of amplifying 2 exons in a conserved domain and their intervening  
 CC intron. The human p53 gene was localised to chromosomal position  
 CC 3q27-29. At least 6 different isoforms exist. Splice variants  
 CC differing at the C-terminus have been designated as alpha, beta and  
 CC gamma forms, while p63 members differing in the N-terminus are  
 CC designated as delta and TA forms, where the delta form lacks the  
 CC transactivation domain. The present sequence represents human  
 CC p63 isoform TAP63 beta. p63 was detected in a variety of  
 CC human and mouse tissue. It demonstrates remarkably divergent  
 CC activities, such as the ability to transactivate p53 reporter genes  
 CC and induce apoptosis. Cessation or down-regulation of p63 expression  
 CC may play a critical role in the process of cervical squamous  
 CC differentiation, both benign and neoplastic. Delta isoforms of p63  
 CC act as dominant negatives towards transactivation by p53 and p63.  
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
 CC cachexia) and neuronal differentiation and related degenerative  
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see  
 CC AAY58572-83) and anti-p63 antibodies of the invention can be used to  
 CC identify compounds useful for treating disorders involving such  
 CC processes, in detection and diagnosis, and in the production of  
 CC transgenic animals.  
 CC  
 SO Sequence 516 AA;  
 Query Match 91.5%; Score 410; DB 20; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 0Y 1 MSQSTQNEFLSPVFOHIMDFLOPICSVOPIDLNFDVDESDGATKIKISMDCTRMQ 60  
 Db 1 MSQSTQNEFLSPVFOHIMDFLOPICSVOPIDLNFDVDESDGATKIKISMDCTRMQ 60

0Y DSDLSDEPMWPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAPQSSSTPDAL 120  
 |||||||  
 Db DSDLSDEPMWPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAPQSSSTPDAL 120  
 0Y 121 SPSPALPSNTDYPGPHSFDSVFOQSSSTAKSATWTYSTELEKLYCOIAKTCPIQIKVMTTP 180  
 |||||||  
 Db 121 SPSPALPSNTDYPGPHSFDSVFOQSSSTAKSATWTYSTELEKLYCOIAKTCPIQIKVMTTP 180  
 0Y 181 POGAVIRAMPYKKAHEHTEVYKRCPNHLSREFNEGIIAPPSHLIRVGNSHQAYVDP 240  
 |||||||  
 Db 181 POGAVIRAMPYKKAHEHTEVYKRCPNHLSREFNEGIIAPPSHLIRVGNSHQAYVDP 240  
 0Y 241 ITGRQSVLPYEPPEOVGTEFTTVLYNFMCSNCSVCGMRRPILITVLETDGQVIGRRC 300  
 |||||||  
 Db 241 ITGRQSVLPYEPPEOVGTEFTTVLYNFMCSNCSVCGMRRPILITVLETDGQVIGRRC 300  
 0Y 301 FEARICACPGDRRADEDSIRKQOVSDSTKNGDGTKRPFQNTHGIOQTSIKRRSPDE 360  
 |||||||  
 Db 301 FEARICACPGDRRADEDSIRKQOVSDSTKNGDGTKRPFQNTHGIOQTSIKRRSPDE 360  
 0Y 361 LLYLPVGRRETYEMILKTKESLELMQYLPQHTIETRYRQOQOQHHLQK 410  
 |||||||  
 Db 361 LLYLPVGRRETYEMILKTKESLELMQYLPQHTIETRYRQOQOQHHLQK 410  
 RESULT 7  
 ID AAB11363 standard; Protein: 516 AA.  
 XX  
 AC AAB11363;  
 XX  
 DE 21-FEB-2001 (first entry)  
 XX  
 PT Human p63 protein isoform #7.  
 XX  
 CC Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
 CC vaccine; detection.  
 KW  
 KW Homo sapiens.  
 OS  
 PN WO200061612-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PF 03-APR-2000; 2000WO-US08896.  
 XX  
 PR 02-APR-1999; 99US-0285479.  
 PR 17-DEC-1999; 99US-0466396.  
 PR 30-DEC-1999; 99US-0476496.  
 PR 10-JAN-2000; 2000US-0480884.  
 PR 22-FEB-2000; 2000US-0510376.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Wang T, Fan L;  
 XX  
 DR WPI: 2000-628399/60.  
 DR N-PSDB: AAC66033.  
 XX  
 PT Isolated polypeptide comprising an immunogenic portion of a lung tumor  
 PT protein is used for detecting and monitoring progression of lung cancer  
 PT in a patient -  
 XX  
 PS Disclosure; Page 255-256; 261pp; English.  
 XX  
 CC This invention describes a novel isolated polypeptide (I) which  
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)  
 CC which have cytostatic activity. The polypeptides and polynucleotides are  
 CC used in compositions and vaccines to inhibit the development of cancer,  
 CC especially lung cancer, in a patient. Methods described in the invention  
 CC can be used to monitor the progression of a cancer by carrying out the  
 CC detection at subsequent time points and comparing the results from a patient  
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient

CC are treated with p2, polynucleotides encoding p2 or antigen presenting  
 CC cells expressing p2 and then administered to the patient to inhibit  
 CC development of cancer.

Sequence 516 AA:

Query Match 91.5%; Score 410; DB 21; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTGTNEFLSEVFOHIMDELEOPICSVOPIDINFEVDESEDAATNKIEISMDCIRMO 60  
 DB 1 MSOSTGTNEFLSEVFOHIMDELEOPICSVOPIDINFEVDESEDAATNKIEISMDCIRMO 60  
 QY 61 DSDLDSPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAAPSPYAPQSSFTDAL 120  
 DB 61 DSDLDSPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAAPSPYAPQSSFTDAL 120  
 QY 121 SPSPAIPSTWDYPGHSHFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180  
 DB 121 SPSPAIPSTWDYPGHSHFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180  
 QY 181 PGAVIRAMPYKKAHEHTEVYKRCPNHELSEFNEGOIAPPSHLIVEGNSHAQYVEDP 240  
 DB 181 PGAVIRAMPYKKAHEHTEVYKRCPNHELSEFNEGOIAPPSHLIVEGNSHAQYVEDP 240  
 QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRC 300  
 DB 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRC 300  
 QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTAKPRFRONTHGIOMTSIKKRRSPDDE 360  
 DB 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTAKPRFRONTHGIOMTSIKKRRSPDDE 360  
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLOK 410  
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLOK 410

RESULT 8  
 ABB74995.

ID ABB74995 standard; Protein: 516 AA.

AC ABB74995;  
 DT 01-MAY-2002 (first entry)  
 DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:344.  
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
 KM immune response.  
 OS Homo sapiens.  
 XX  
 PN WO200200174-A2.  
 PD 03-JAN-2002.  
 PF 28-JUN-2001; 2001MO-US21065.  
 PR 28-JUN-2000; 2000US-0606421.  
 PR 02-AUG-2000; 2000US-0630940.  
 PR 21-AUG-2000; 2000US-0643597.  
 PR 15-SEP-2000; 2000US-0662786.  
 PR 09-OCT-2000; 2000US-0685696.  
 PR 12-DEC-2000; 2000US-0735705.  
 PR 07-MAY-2001; 2001US-0850716.

(CORI-) CORIXA CORP.

Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;  
 PI McNeill PD, Fanger N, Retler MW, Marnierakis M, Fanger GR;  
 PI Vedrick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI: 2002-090513/12.  
 DR N-PSDB: ABL49252.

Polynucleotides encoding lung tumor polypeptides, useful for treating  
 lung cancer or stimulating an immune response -  
 Example 2; Page 327-328; 374pp; English.

The present invention describes human lung tumour proteins. Human lung  
 tumour proteins and polynucleotides have cytostatic and immunostimulant  
 activities, and can be used in vaccine production. Compositions  
 comprising the lung tumour proteins, polynucleotides, antibodies,  
 fusion proteins, T cell populations, or antigen presenting cells that  
 express the lung tumour proteins are useful for treating lung cancer or  
 stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to  
 ABB75070 represent sequences used in the exemplification of the present  
 invention.

Sequence 516 AA:

Query Match 91.5%; Score 410; DB 23; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTGTNEFLSEVFOHIMDELEOPICSVOPIDINFEVDESEDAATNKIEISMDCIRMO 60  
 DB 1 MSOSTGTNEFLSEVFOHIMDELEOPICSVOPIDINFEVDESEDAATNKIEISMDCIRMO 60  
 QY 61 DSDLDSPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAAPSPYAPQSSFTDAL 120  
 DB 61 DSDLDSPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAAPSPYAPQSSFTDAL 120  
 QY 121 SPSPAIPSTWDYPGHSHFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180  
 DB 121 SPSPAIPSTWDYPGHSHFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180  
 QY 181 PGAVIRAMPYKKAHEHTEVYKRCPNHELSEFNEGOIAPPSHLIVEGNSHAQYVEDP 240  
 DB 181 PGAVIRAMPYKKAHEHTEVYKRCPNHELSEFNEGOIAPPSHLIVEGNSHAQYVEDP 240  
 QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRC 300  
 DB 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCVGNNRRPILIIYVLETRDQVGLRRC 300  
 QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTAKPRFRONTHGIOMTSIKKRRSPDDE 360  
 DB 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTAKPRFRONTHGIOMTSIKKRRSPDDE 360  
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLOK 410  
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLOK 410

RESULT 9

ID AAY45247 standard; Protein: 641 AA.

AC AAY45247;  
 DT 07-JAN-2000 (first entry)  
 DE Human p51 protein B.  
 KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;  
 KM tumour suppression; diagnosis.  
 OS Homo sapiens.

Key Location/Qualifiers  
 FT Domain 1..59  
 FT Domain /label= transactivation\_domain  
 FT Domain 142..321

	/label= DNA_binding_domain
	353..397
	/label= oligomerisation_domain
FT	Domain
FN	M09950412-AI.
PX	07-OCT-1999.
XX	
PD	
PE	24-MAR-1999;   99WO-JP01512.
PR	27-MAR-1998;   98JP-0100467.
PA	(SAKA.) OTSUKA PHARM CO LTD. (IKAW/) IKAMA Y.
PI	Ikawa Y, Ikawa S, Obinata M;
DR	WPJ: 1999-591318/50.
N-	PSDB: AAZ25771.
PT	New p53 related human gene p5l, useful for diagnosis, investigation and treatment of cancers and screening for potential cell proliferation agents -
XX	
XX	Example I: Page 152-154; 163pp; Japanese.
CC	The present sequence represents a human p5l protein, which is related to
CC	p53 and has cell proliferation regulation and tumour suppression
CC	activity. The p5l gene can be used in the investigation, diagnosis and
CC	treatment of diseases such as cancer, with which the p53 family cell
CC	proliferation regulation is associated. The p5l protein may be used for
CC	screening potential agonists and antagonists of its regulatory function,
CC	for use as drugs,
SQ	Sequence     641 AA;
	Query Match       91.5%; Score 410; DB 20; Length 641; Best Local Similarity 100.0%; Pred. No. 0; Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	MSOSTGTNEFISPEVFOHIMPLDEOPICSVPIDLNFVDSESDATNKIELSMCIRMQ 60
DB	MSSTQTNEFLSPFEFHIMPDLLEOPICSVOPIDLPVEDPEDGATNKLIEISMCIHQ 60
OY	DSDLSDDPMWPOYTNLGLNSMDQQIQNGSSSTRPYNTDHAQNVSVTAPSPYAOPSFFDAL 120
DB	DSDLSDPMWPOYTNLGLNSMDQQIQNGSSSTRPYNTDHAQNVSVTAPSPYAOPSFFDAL 120
OY	SPSPAIPSNITDPGHSHFDVSFSOOSSIAKSATWTYSTELIKLYCOIAKTCPIDQIKMTPP 180
DB	SPSPAIPSNITDPGHSHFDVSFSOOSSIAKSATWTYSTELIKLYCOIAKTCPIDQIKMTPP 180
OY	PGGVAVIRMAMPYYKKAEHTVEVKRCRPNHELRSHEFGOGAPPSSHILRVGNSHAQVDEP 240
DB	PGAGVAVIRMAMPYYKKAEHTVEVKRCRPNHELRSHEFGOGAPPSSHILRVGNSHAQVDEP 240
OY	ITQGOSVLVPREPDOVGTEFTTVLVYNEMCNSSCVGMNRRLIIIVTLETTRDGQYLGRRC 300
DB	ITTGROSLVLPREPVGGTEFTTVLVYNFMKNSSCGVMNRRLIIIVTLETTRDGQYLGRRC 300
OY	PEARICACPGDRADDEDISKNOOVSDSTKGNDGKRPPROMTHGIOMTSIKRRSPDDE 360
DB	PEARICACPGDKRADEDISKNOOVSDSTKGNDGKRPPROMTHGIOMTSIKRRSPDDE 360
OY	LVIYPVRGRETYEMLLIKIESILELMQVLPQHITIETRYROOOQOOHOHLLOK 410
DB	LVIYPVRGRETYEMLLIKIESILELMQVLPQHITIETRYROOOQOOHOHLLOK 410
RESULT 10	
AAY05953	standard; Protein: 641 AA.

AC		AAV05953;	
XX		16-AUG-1999	(first entry)
DT			
XX			
DE		Human cell regulatory protein p63, isoform hUTAP63 alpha.	
XX			
KM		Cell regulatory protein; p63; hUTAP63 alpha; TP63 alpha; human;	
KW		cancer; tumour suppressor; cell cycle control; apoptosis;	
RW		cell proliferation; cell differentiation; therapy.	
XX			
OS		Homo sapiens.	
XX			
PN		W09919357-A2.	
XX			
PD		22-APR-1999.	
PF		02-OCT-1998;	98WO-US2192.
XX			
FR		29-MAY-1998;	98US-0087215.
PR		15-OCT-1997;	97US-0062076.
PA		(HARD ) HARVARD COLLEGE.	
XX			
EI		McKeon F, Yang A;	
DR		WP1; 1999-277595/23.	
DR		N-PSDB; AAX58572.	
XX			
PT		New isolated p63 cell regulatory protein for, e.g. treatment of	
PT		tumours	
XX			
XX		Claim 23; Fig 9; 161pp; English.	
CC		The present invention concerns the discovery of a new family of	
CC		cell regulatory proteins (CRPs) termed the p63 family of proteins,	
CC		which demonstrate certain sequence identity to known tumour	
CC		suppressor proteins p53 and p73. It has been observed that the	
CC		intron-exon organisation is conserved between p73 and p53, and from	
CC		known exon and intron sizes for these 2 genes, it was possible to	
CC		identify new members of this gene family using a PCR-based strategy	
CC		of amplifying 2 exons in a conserved domain and their intervening	
CC		intron. The human p53 gene was localised to chromosomal position	
CC		3q27-29. At least 6 different isotypes exist. Splice variants	
CC		differing at the C-terminus have been designated as alpha, beta and	
CC		gamma forms, while p63 members differing in the N-terminus are	
CC		designated as delta and TA forms, where the delta form lacks the	
CC		transactivation domain. The present sequence represents human	
CC		p63 isotype TAp63 alpha. p63 was detected in a variety of	
CC		human and mouse tissue. It demonstrates remarkably divergent	
CC		activities, such as the ability to transactivate p53 reporter genes	
CC		and induce apoptosis. Cessation or down-regulation of p63 expression	
CC		may play a critical role in the process of cervical squamous	
CC		differentiation, both benign and neoplastic. Delta isotopes of p63	
CC		act as dominant negatives towards transactivation by p53 and p63.	
CC		p63 may also be implicated in haematopoiesis, muscle wasting (e.g.	
CC		cachexia) and neuronal differentiation and related degenerative	
CC		disorders. p63 polypeptides (see AAV05953-64), polynucleotides (see	
CC		AAX58572-83) and anti-p63 antibodies of the invention can be used to	
CC		identify compounds useful for treating disorders involving such	
CC		processes, in detection and diagnosis, and in the production of	
CC		transgenic animals.	
CC			
SQ	Sequence	641 AA;	
	Query Match	91.5%; Score 410; DB 20; Length 641;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 410; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
OY	1 MSOSTGTNEFLSPEVFQHTWDFLEDPICSVOPIDLNLFVDEPSEDGATNKIEISMDCIRMQ	60	
Dd	1 MSOSTGTNEFLSPEVFQHTWDFLEDPICSVOPIDLNLFVDEPSEDGATNKIEISMDCIRMQ	60	
OY	61 DSDLSDDPMPOYTNLGLNMSDQOIONCSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL	120	

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Db      61 DSDLSDDPMWPOYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
OY      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
OY      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
OY      241 ITGRQSVLYVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLYGRRC 300
Db      241 ITGRQSVLYVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLYGRRC 300
OY      301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKKRRSPDDE 360
Db      301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKKRRSPDDE 360
OY      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLOK 410
Db      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLOK 410

RESULT 11
AAB11358
ID      AAB11358 standard; protein; 641 AA.
XX
AC      AAB11358;
XX
DT      21-FEB-2001 (first entry)
XX
DE      Human p63 protein isoform #2.
XX
KW      Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX      vaccine; detection.
XX
OS      Homo sapiens.
XX
PN      WO200061612-A2.
XX
PD      19-OCT-2000.
XX
PF      03-APR-2000; 2000WO-US08896.
XX
PR      02-APR-1999; 99US-0285479.
XX      17-DEC-1999; 99US-0466396.
XX      30-DEC-1999; 99US-0476496.
XX      10-JAN-2000; 2000US-0480884.
XX      22-FEB-2000; 2000US-0510376.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Wang T, Fan L;
XX
DR      WPI; 2000-628399/60.
XX      N-PSDB; AAC66028.
XX
PT      Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT      protein is used for detecting and monitoring progression of lung cancer
PT      in a patient.
XX
PS      Disclosure; Page 245-247; 261pp; English.
XX
CC      This invention describes a novel isolated polypeptide (I) which
CC      comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC      which have cytostatic activity. The polypeptides and polynucleotides are
CC      used in compositions and vaccines to inhibit the development of cancer,
CC      especially lung cancer, in a patient. Methods described in the invention
CC      can be used to monitor the progression of a cancer by carrying out the
CC      detection at subsequent time points and comparing the results from the
CC      different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC      are treated with P2, polynucleotides encoding P2 or antigen presenting

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CC      Cells expressing P2 and then administered to the patient to inhibit
CC      development of cancer.
XX
SQ      Sequence      641 AA;
XX
Query Match      91.5%; Score 410; DB 21; Length 641;
Best local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 MSOSTQNEFLSPVFOHIMDFLEQPCISVQPIDLNFVDPSPDGAATNKIEIMDCIRMQ 60
Db      1 MSOSTQNEFLSPVFOHIMDFLEQPCISVQPIDLNFVDPSPDGAATNKIEIMDCIRMQ 60
OY      61 DSDLSDDPMWPOYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db      61 DSDLSDDPMWPOYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
OY      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSPFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
OY      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 POGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
OY      241 ITGRQSVLYVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLYGRRC 300
Db      241 ITGRQSVLYVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLYGRRC 300
OY      301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKKRRSPDDE 360
Db      301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKKRRSPDDE 360
OY      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLOK 410
Db      361 LTYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLOK 410

RESULT 12
AAB82129
ID      AAB82129 standard; protein; 641 AA.
XX
AC      AAB82129;
XX
DT      03-AUG-2001 (first entry)
XX
DE      Human protein #2 used to produce a chimeric p53 protein.
XX
KW      Human; cytostatic; gene therapy; p53; human tumour.
XX
OS      Homo sapiens.
XX
PI      Key
XX      Location/Qualifiers
XX      1..59
XX      Domain /label= Transactivation_domain
XX      142..321
XX      Domain /label= DNA_binding_domain
XX      353..397
XX      Domain /label= Oligomerisation_domain
XX
PN      JP2000354488-A.
XX
PD      26-DEC-2000.
XX
PF      09-APR-1999; 99JP-0139034.
XX
PR      09-APR-1999; 99JP-0139034.
XX
PA      (IKAW/) IKAWA H.
XX      (SAKA ) OTSUKA PHARM CO LTD.
XX
DR      WPI; 2001-268293/28.
XX      N-PSDB; AAF86589.

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XX Chimera gene of the p53 family, useful for gene therapy, and treatment  
 PT of cancer, comprises a transcription activating region and a DNA  
 PT binding region -

XX Example 1; Page 37-40; 57pp; Japanese.

XX The present invention relates to a chimera gene of p53 family encoding a  
 CC transcription activating region, a DNA binding region, and an oligomer  
 CC formation region of different p53 family proteins. The chimeric gene can  
 CC be used for gene therapy of p53 variant human tumours, and analysis of  
 CC the function of the p53 family gene. The present sequence was used in the  
 CC present invention.

XX Sequence 641 AA;

Query Match 91.5%; Score 410; DB 22; Length 641;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTFNEFLSPYFQHIWDFLEOPICSVOPIDLNFDVDESEDCATKIEISMDCIRMQ 60  
 DB 1 MSOSTQTFNEFLSPYFQHIWDFLEOPICSVOPIDLNFDVDESEDCATKIEISMDCIRMQ 60  
 QY 61 DSDSDPMPWPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVAPSPYAPSSSTFDAL 120  
 DB 61 DSDSDPMPWPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVAPSPYAPSSSTFDAL 120  
 QY 121 SPSPAIPSNTDYPGPHSFDSVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180  
 DB 121 SPSPAIPSNTDYPGPHSFDSVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180  
 QY 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGOIAPPSHLIRVGNSHAQYVDP 240  
 DB 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGOIAPPSHLIRVGNSHAQYVDP 240  
 QY 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300  
 DB 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300  
 QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDE 360  
 DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDE 360  
 QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQK 410  
 DB 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQK 410

RESULT 13

ABB74990 ID ABB74990 standard; Protein; 641 AA.

XX ABB74990;

XX 01-MAY-2002 (first entry)

DE Human p53 homologue isoform, p63 (L530S). protein SEQ ID NO:339.

XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
 KW immune response.

XX Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.  
 PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.  
 PR 09-OCT-2000; 2000US-0685696.  
 PR 12-DEC-2000; 2000US-0735705.  
 PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;  
 PI McNeill PD, Fanger N, Retter MW, Marinakis M, Fanger GR;  
 PI Veddyk TS, Carter D, Watanabe Y, Peckham DW;

XX WPI: 2002-090513/12.

DR N-PSDB: ABL49247.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating  
 PT lung cancer or stimulating an immune response -

XX Example 2; Page 321-322; 374pp; English.

CC The present invention describes human lung tumor proteins. Human lung  
 CC tumor proteins and polynucleotides have cytostatic and immunostimulant  
 CC activities, and can be used in vaccine production. Compositions  
 CC comprising the lung tumor proteins, polynucleotides, antibodies,  
 CC fusion proteins, T cell populations, or antigen presenting cells that  
 CC express the lung tumor proteins are useful for treating lung cancer or  
 CC stimulating an immune response. ABL4959 to ABL49300 and ABB74946 to  
 CC ABB75070 represent sequences used in the exemplification of the present  
 CC invention.

XX Sequence 641 AA;

Query Match 91.5%; Score 410; DB 23; Length 641;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTFNEFLSPYFQHIWDFLEOPICSVOPIDLNFDVDESEDCATKIEISMDCIRMQ 60  
 DB 1 MSOSTQTFNEFLSPYFQHIWDFLEOPICSVOPIDLNFDVDESEDCATKIEISMDCIRMQ 60  
 QY 61 DSDSDPMPWPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVAPSPYAPSSSTFDAL 120  
 DB 61 DSDSDPMPWPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVAPSPYAPSSSTFDAL 120  
 QY 121 SPSPAIPSNTDYPGPHSFDSVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180  
 DB 121 SPSPAIPSNTDYPGPHSFDSVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180  
 QY 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGOIAPPSHLIRVGNSHAQYVDP 240  
 DB 181 POGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGOIAPPSHLIRVGNSHAQYVDP 240  
 QY 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300  
 DB 241 ITGROSIVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMRRPILIIIVLETRDGOVLGRRC 300  
 QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDE 360  
 DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDE 360  
 QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQK 410  
 DB 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQK 410

RESULT 14

AAB11361 ID AAB11361 standard; Protein; 680 AA.

XX AAB11361;

XX 21-FEB-2001 (first entry)

DE Human p63 protein isoform #5.



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OY      181 POGAVIRAMPVYKKAHVEYVKRCPNHLSRPFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
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Db      220 POGAVIRAMPVYKKAHVEYVKRCPNHLSRPFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
      |||||||
OY      241 ITGROSVLVPEPPPOVGETTEVTLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVLGRRC 300
      |||||||
Db      280 ITGROSVLVPEPPPOVGETTEVTLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVLGRRC 339
      |||||||
OY      301 FEARICACPRGRKADSDSIRKQOVSSTKNGDGTTRPRONTGCIQMTSIKKRRSPDDE 360
      |||||||
Db      340 FEARICACPRGRKADSDSIRKQOVSSTKNGDGTTRPRONTGCIQMTSIKKRRSPDDE 399
      |||||||
OY      361 LLYLPVGRREYEMLIKIKESLELMQYLPQHTIETTYROOOOHOHLQK 410
      |||||||
Db      400 LLYLPVGRREYEMLIKIKESLELMQYLPQHTIETTYROOOOHOHLQK 449
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Search completed: June 24, 2003, 22:25:49  
 Job time : 40 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2003, 22:11:01 ; Search time 26 Seconds  
(without alignments)  
1864.487 Million cell updates/sec

Title: US-09-670-568B-1  
Perfect score: 448  
Sequence: 1 MSQSTQTNFLSPVFGH.....PKQSDVFRHKKPNRSVYP 448

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 417779 seqs, 108206813 residues

Word size : 0

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	448	10	US-09-735-705-340
2	448	100.0	448	10	US-09-850-716A-340
3	448	100.0	448	10	US-09-897-778-340
4	410	91.5	516	10	US-09-735-705-344
5	410	91.5	516	10	US-09-850-716A-344
6	410	91.5	516	10	US-09-897-778-344
7	410	91.5	641	10	US-09-735-705-339
8	410	91.5	641	10	US-09-850-716A-339
9	410	91.5	641	10	US-09-897-778-339
10	410	91.5	680	10	US-09-735-705-342
11	410	91.5	680	10	US-09-850-716A-342
12	410	91.5	680	10	US-09-897-778-342
13	341	76.1	461	10	US-09-735-705-343
14	341	76.1	461	10	US-09-850-716A-343
15	341	76.1	461	10	US-09-897-778-343
16	272	60.7	586	10	US-09-735-705-338
17	272	60.7	586	10	US-09-850-716A-338
18	272	60.7	586	10	US-09-897-778-338
19	269	60.0	356	10	US-09-735-705-341

20	269	60.0	356	10	US-09-850-716A-341	Sequence 341, App
21	269	60.0	356	10	US-09-897-778-341	Sequence 341, App
22	191	42.6	586	10	US-09-735-705-152	Sequence 152, App
23	191	42.6	586	10	US-09-850-716A-152	Sequence 152, App
24	191	42.6	586	10	US-09-897-778-152	Sequence 152, App
25	22	4.9	635	12	US-10-155-059-3	Sequence 3, Appli
26	22	4.9	636	10	US-09-732-384-10	Sequence 10, Appli
27	9	2.0	71	9	US-10-007-557-9	Sequence 9, Appli
28	9	2.0	271	10	US-09-925-302-680	Sequence 680, App
29	9	2.0	293	10	US-09-968-958-2	Sequence 2, Appli
30	9	2.0	293	10	US-09-968-958-4	Sequence 4, Appli
31	9	2.0	319	9	US-09-968-851-42	Sequence 42, Appl
32	9	2.0	335	9	US-09-968-851-44	Sequence 44, Appl
33	9	2.0	353	9	US-09-968-851-40	Sequence 40, Appl
34	9	2.0	353	9	US-10-146-473-78	Sequence 78, Appl
35	9	2.0	363	9	US-09-968-851-26	Sequence 26, Appl
36	9	2.0	374	9	US-09-968-851-48	Sequence 28, Appl
37	9	2.0	381	9	US-09-968-851-36	Sequence 36, Appl
38	9	2.0	390	9	US-10-038-010-6	Sequence 6, Appli
39	9	2.0	393	9	US-09-029-327-4	Sequence 4, Appli
40	9	2.0	393	9	US-09-860-286-9	Sequence 9, Appli
41	9	2.0	393	10	US-09-776-695-32	Sequence 32, Appl
42	9	2.0	393	10	US-09-732-384-3	Sequence 3, Appli
43	9	2.0	393	10	US-09-860-211-9	Sequence 9, Appli
44	9	2.0	394	12	US-10-155-059-4	Sequence 4, Appli
45	9	2.0	401	9	US-09-968-851-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1  
US-09-735-705-340  
; Sequence 340, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Lique  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 340  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-340

Query Match	100.0%	Score 448;	DB 10;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MSQSTQTNFLSPVFGHINDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ	60	
Qy	61	DSDSLDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL	120	
Db	61	DSDSLDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL	120	

QY 121 SPSPAIPTNDYPCPHSFDFVFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180  
Db 121 SPSPAIPTNDYPCPHSFDFVFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180  
QY 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
Db 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
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Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 300  
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Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360  
QY 361 LLYLPVGRGTYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420  
Db 361 LLYLPVGRGTYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420  
QY 421 LVEPRETPKQSDVFFRHSKPPNRSVYP 448  
Db 421 LVEPRETPKQSDVFFRHSKPPNRSVYP 448

## RESULT 2

US-09-850-716A-340  
; Sequence 340, Application US/09850716A  
; Patent No. US20020115139A1  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 340  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-340

Query Match 100.0%; Score 448; DB 10; Length 448;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MSQSTQNEFLSPVFOHIDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCI 60  
QY 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
Db 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
QY 121 SPSPAIPSTNDYPCPHSFDFVFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180  
Db 121 SPSPAIPSTNDYPCPHSFDFVFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180  
QY 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
Db 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 300  
Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 300  
QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360  
Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360

QY 361 LLYLPVGRGTYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420  
Db 361 LLYLPVGRGTYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420  
QY 421 LVEPRETPKQSDVFFRHSKPPNRSVYP 448  
Db 421 LVEPRETPKQSDVFFRHSKPPNRSVYP 448

## RESULT 3

US-09-897-778-340  
; Sequence 340, Application US/09897778  
; Patent No. US20020147143A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 340  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-340

Query Match 100.0%; Score 448; DB 10; Length 448;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
Db 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
QY 121 SPSPAIPSTNDYPCPHSFDFVFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180  
Db 121 SPSPAIPSTNDYPCPHSFDFVFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180  
QY 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
Db 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDQGVLGRR 300  
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Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360  
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Db 361 LLYLPVGRGTYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKLLSACFRNE 420  
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Db 421 LVEPRETPKQSDVFFRHSKPPNRSVYP 448

## RESULT 4

US-09-735-705-344  
; Sequence 344, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 344  
; LENGTH: 516  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-344

Query Match 91.5%; Score 410; DB 10; Length 516;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSQSTQTNFELSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIISMDCIRMQ 60
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DB 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 300
DB 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 300
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
DB 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQOHHLLQK 410
DB 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQOHHLLQK 410
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## RESULT 5

US-09-850-716A-344  
; Sequence 344, Application US/09850716A  
; Patent No. US20020115139A1  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 344  
; LENGTH: 516  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-344

Query Match 91.5%; Score 410; DB 10; Length 516;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSQSTQTNFELSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIISMDCIRMQ 60
DB 1 MSQSTQTNFELSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIISMDCIRMQ 60
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
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DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 300
DB 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 300
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
DB 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQOHHLLQK 410
DB 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIYRQOOOQOHHLLQK 410
```

## RESULT 6

US-09-897-778-344  
; Sequence 344, Application US/09897778  
; Patent No. US20020147143A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darriek  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 344  
; LENGTH: 516  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-344

Query Match 91.5%; Score 410; DB 10; Length 516;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60  
DB 1 MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

QY 61 DSDLSDDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
DB 61 DSDLSDDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180  
DB 121 SPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180

QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
DB 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240

QY 241 ITRQSVLVPYEPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC 300  
DB 241 ITRQSVLVPYEPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC 300

QY 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDE 360  
DB 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDE 360

QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETVROOOOQOHHLLQK 410  
DB 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETVROOOOQOHHLLQK 410

## RESULT 7

US-09-735-705-339  
; Sequence 339, Application US/09735705  
; Patent No. US20020052329A1

## GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.

## TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C14

; CURRENT APPLICATION NUMBER: US/09/735,705

; CURRENT FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 419

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 339

; LENGTH: 641

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-735-705-339

Query Match 91.5%; Score 410; DB 10; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60  
DB 1 MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

QY 61 DSDLSDDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
DB 61 DSDLSDDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180  
DB 121 SPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180

QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
DB 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240

QY 241 ITRQSVLVPYEPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC 300  
DB 241 ITRQSVLVPYEPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC 300

QY 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDE 360  
DB 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDE 360

QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETVROOOOQOHHLLQK 410  
DB 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETVROOOOQOHHLLQK 410

## RESULT 8

US-09-850-716A-339  
; Sequence 339, Application US/09850716A  
; Patent No. US20020115139A1

## GENERAL INFORMATION:

; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.

; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C15

; CURRENT APPLICATION NUMBER: US/09/850,716A

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 339

; LENGTH: 641

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-850-716A-339

Query Match 91.5%; Score 410; DB 10; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60  
DB 1 MSQSTQTNFLSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

QY 61 DSDLSDDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
DB 61 DSDLSDDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180  
DB 121 SPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180

QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
DB 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240

QY 241 ITRQSVLVPYEPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC 300  
DB 241 ITRQSVLVPYEPQVGTFTVLYNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRC 300

QY 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDE 360  
DB 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPFQNTGHIQMTSIKKRRSPDDE 360

QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETVROOOOQOHHLLQK 410  
DB 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETVROOOOQOHHLLQK 410

Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQQHLLQK 410

RESULT 9

US-09-897-778-339  
 ; Sequence 339, Application US/09897778  
 ; Patent No. US20020147143A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Manerakis, Margarita  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Vedrick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Peckham, David W.  
 ; APPLICANT: Fanger, Neil  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.455C16  
 ; CURRENT APPLICATION NUMBER: US/09/897,778  
 ; CURRENT FILING DATE: 2001-06-28  
 ; NUMBER OF SEQ ID NOS: 467  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 339  
 ; LENGTH: 641  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-897-778-339

Query Match 91.5%; Score 410; DB 10; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSQSTQTFNEFLSPVQFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60  
 Db 1 MSQSTQTFNEFLSPVQFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60  
 QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSTFDAL 120  
 Db 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSTFDAL 120  
 QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 180  
 Db 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 180  
 QY 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
 Db 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
 QY 241 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 300  
 Db 241 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 300  
 QY 301 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 360  
 Db 301 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 360  
 QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQQHLLQK 410  
 Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQQHLLQK 410

RESULT 10

US-09-735-705-342  
 ; Sequence 342, Application US/09735705  
 ; Patent No. US20020052329A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Fan, Liqun  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Li, Samuel X.  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Fanger, Neil  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.455C14  
 ; CURRENT APPLICATION NUMBER: US/09/735,705  
 ; CURRENT FILING DATE: 2000-12-12  
 ; NUMBER OF SEQ ID NOS: 419  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 342  
 ; LENGTH: 680  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-735-705-342

Query Match 91.5%; Score 410; DB 10; Length 680;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSQSTQTFNEFLSPVQFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60  
 Db 40 MSQSTQTFNEFLSPVQFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99  
 QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSTFDAL 120  
 Db 100 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSTFDAL 159  
 QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 180  
 Db 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 219  
 QY 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
 Db 220 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279  
 QY 241 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 300  
 Db 280 ITGRQSVLPVPEPPQVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 339  
 QY 301 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 360  
 Db 340 FEARICAPGRDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIOMTSIKKRSPDDE 399  
 QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQQHLLQK 410  
 Db 400 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQQHLLQK 449

RESULT 11

US-09-850-716A-342  
 ; Sequence 342, Application US/09850716A  
 ; Patent No. US20020115139A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Retter, Marc W.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.455C15  
 ; CURRENT APPLICATION NUMBER: US/09/850,716A  
 ; CURRENT FILING DATE: 2001-05-07  
 ; NUMBER OF SEQ ID NOS: 440  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 342  
 ; LENGTH: 680  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-850-716A-342

Query Match  
Best Local Similarity 91.5%; Score 410; DB 10; Length 680;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60  
Db 40 MSQSTQTNFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 99  
QY 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
Db 100 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159  
QY 121 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180  
Db 160 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219  
QY 181 PGAVIRAMPYVYKKAHVTEVVKRCPNHLSREFNEQIAPPSSHILIRVEGNSHAQYVEDP 240  
Db 220 PGAVIRAMPYVYKKAHVTEVVKRCPNHLSREFNEQIAPPSSHILIRVEGNSHAQYVEDP 279  
QY 241 ITGRQSVLPVPEPPQVGTETTTVLNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 300  
Db 280 ITGRQSVLPVPEPPQVGTETTTVLNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 339  
QY 301 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360  
Db 340 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 399  
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQK 410  
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQK 449

RESULT 12  
US-09-897-778-342  
; Sequence 342, Application US/09897778  
; Patent No. US20020147143A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Warnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darriek  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 342  
; LENGTH: 680  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-342

Query Match  
Best Local Similarity 91.5%; Score 410; DB 10; Length 680;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60  
Db 40 MSQSTQTNFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 99  
QY 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
Db 100 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

QY 121 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180  
Db 160 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219  
QY 181 PGAVIRAMPYVYKKAHVTEVVKRCPNHLSREFNEQIAPPSSHILIRVEGNSHAQYVEDP 240  
Db 220 PGAVIRAMPYVYKKAHVTEVVKRCPNHLSREFNEQIAPPSSHILIRVEGNSHAQYVEDP 279  
QY 241 ITGRQSVLPVPEPPQVGTETTTVLNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 300  
Db 280 ITGRQSVLPVPEPPQVGTETTTVLNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRR 339  
QY 301 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360  
Db 340 FEARICACGRDKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 399  
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQK 410  
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQK 449

RESULT 13  
US-09-735-705-343  
; Sequence 343, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Ligu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 343  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-343

Query Match  
Best Local Similarity 76.1%; Score 341; DB 10; Length 461;  
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129  
Db 15 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74  
QY 130 TDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTPPOGAVIRAM 189  
Db 75 TDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTPPOGAVIRAM 134  
QY 190 PVYKKAHVTEVVKRCPNHLSREFNEQIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV 249  
Db 135 PVYKKAHVTEVVKRCPNHLSREFNEQIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV 194  
QY 250 PYEPQVGTETTTVLNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRCFEACAP 309  
Db 195 PYEPQVGTETTTVLNFMCMNSCVCVGMNRRPILIIIVTLETRDGOVLGRRCFEACAP 254  
QY 310 GRORKADEDSIRKQOVSSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDELLYLPVGR 369

Db 255 GRDRKADEDSIRKQOYSDSTKNGDGTGRPFQNTGHIQMTSIIKRRSPDDELLYLPVGR 314  
QY 370 ETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 410  
Db 315 ETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 355

RESULT 14  
US-09-850-716A-343  
; Sequence 343, Application US/09850716A  
; Patent No. US20020115139A1  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 343  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-850-716A-343

Query Match 76.1%; Score 341; DB 10; Length 461;  
Best Local Similarity 100.0%; Pred. No. 4.9e-311;  
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129  
Db 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74  
QY 130 TDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189  
Db 75 TDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 134  
QY 190 PVYKKAHVTEVVKRCNPHELSEFNEGQIAPPESHILIRVEGNSHAQYVEDPITGRQSVLV 249  
Db 135 PVYKKAHVTEVVKRCNPHELSEFNEGQIAPPESHILIRVEGNSHAQYVEDPITGRQSVLV 194  
QY 250 PYEPPQVGTFTVLVNFMCNCSVCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 309  
Db 195 PYEPPQVGTFTVLVNFMCNCSVCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254  
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RESULT 15  
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; Sequence 343, Application US/09897778  
; Patent No. US2002014743A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Warnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 343  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-343

Query Match 76.1%; Score 341; DB 10; Length 461;  
Best Local Similarity 100.0%; Pred. No. 4.9e-311;  
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QY 130 TDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189  
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Search completed: June 24, 2003, 22:24:22  
Job time : 28 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 07:58:28 ; Search time 3502 Seconds  
(without alignments)  
13022.984 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estnu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_hic.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_hic.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
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- 19: em\_gss\_inv.\*
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- 22: em\_gss\_fun.\*
- 23: em\_gss\_mam.\*
- 24: em\_gss\_mus.\*
- 25: em\_gss\_other.\*
- 26: em\_gss\_pro.\*
- 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c 9	284	10.1	517	10	AW382125	AW382125	CMO-HT032
c 10	275	9.8	498	9	AI809318	AI809318	we96a04.x
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c 20	195	6.9	379	10	AW382639	AW382639	PM0-HT033
c 21	163	5.8	341	10	AW382607	AW382607	PM0-HT033
c 22	161	5.7	412	12	BE706715	BE706715	PM0-HT033
c 23	154	5.5	507	10	AW382186	AW382186	CMO-HT032
c 24	151	5.4	371	10	AW382671	AW382671	PM0-HT033
c 25	143	5.1	405	12	BE706691	BE706691	PM0-HT033
c 26	137	4.9	400	10	AW382589	AW382589	PM0-HT033
c 27	101	3.6	429	10	AW379322	AW379322	MR0-HT024
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ALIGNMENTS

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VERSION	BM477989.1	GI:18527031			
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SOURCE	human.				
ORGANISM	Homo sapiens				
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AUTHORS	1 (bases 1 to 1042)				
TITLE	NIH-MGC http://mgi.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Lou Staudt CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: Agencourt Bioscience Corporation found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM12268 row: d column: 20 High quality sequence stop: 660. Location/Qualifiers 1. .1042				
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source					



AL698768  
AL698768.1 GI:19619308  
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SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (bases 1 to 563)  
AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Weill, B. and Wiemann, S.  
TITLE EST (Wambutt, R., Heubner, D., Mewes, H.W., Weill, B. and Wiemann, S.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Wambutt R  
MIPS  
Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686H1410) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
FEATURES  
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AL698769  
AL698769.1  
EST 21-MAR-2002

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ACCESSION AL698769  
VERSION AL698769.1 GI:19619309  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (bases 1 to 563)  
AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Weill, B. and Wiemann, S.  
TITLE EST (Wambutt, R., Heubner, D., Mewes, H.W., Weill, B. and Wiemann, S.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Wambutt R  
MIPS  
Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686H1810) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
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Best Local Similarity 100.0%; Pred. No. 4e-178;  
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ACCESSION AW368377
VERSION AW368377.1 GI:6873027
KEYWORDS EST.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 636)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&td=PM2-HT0190-081099-001-c08&t3=1999-10-08&t4=1)
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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VERSION AW368375.1 GI:6873025
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
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low stringency conditions."
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172 a 73 c 100 g 153 t

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QY 2378 GCCCTCTCACAAAATCTGTGATTAATTGCTTAATAGAGCTTCTATCCCTCAAGCCCTAC 2437  
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DB 438 GCCCTCTCACAAAATCTGTGATTAATTGCTTAATAGAGCTTCTATCCCTCAAGCCCTAC 379  
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QY 2438 CTACATAAACCAGCAGCATATCTAGTACTGTTTCAGTCGATTTAGCCAGAGACTTACG 2497  
|||||  
DB 378 CTACATAAACCAGCAGCATATCTAGTACTGTTTCAGTCGATTTAGCCAGAGACTTACG 319  
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QY 2498 TTTTGAGTAACTGAGATCCAGCAGACGTGTTAAATCAGCAGCTCCTGGACTGGAAATTA 2557  
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DB 318 TTTTGAGTAACTGAGATCCAGCAGACGTGTTAAATCAGCAGCTCCTGGACTGGAAATTA 259  
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QY 2558 AAGATTGAAGGGTAGACTACTTTTCTTTTAAAA 2592  
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DB 258 AAGATTGAAGGGTAGACTACTTTTCTTTTAAAA 224  
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RESULT 11  
BE145042  
LOCUS 293 bp mRNA linear EST 21-JUN-2000  
DEFINITION PM4-HT0191-281099-002-c10 HT0191 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE145042  
VERSION BE145042.1 GI:8607766  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 293)  
REFERENCE  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.J.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

## Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=6t2-PM4-HT0191-281099-002-c10&t3=1999-10-28&t4=1)  
Seq primer: puc 18 forward  
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Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/dev\_stage="Adult"  
/note="Organ: head/neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
77 a 59 c 65 g 92 t

BASE COUNT 77 a 59 c 65 g 92 t  
ORIGIN

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Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 37 GATCATTTACCAAAAGTAATCAACTTTGTGGGTGGAGAGTTCTTTGTGAGAACTTGCATTA 96  
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QY 2120 TTTGTGTCCTCCCTCATGTGTAGTAGAACAATTTCTTAATGCTGTGTACCTGCTCTGC 2179  
|||||  
DB 97 TTTGTGTCCTCCCTCATGTGTAGTAGAACAATTTCTTAATGCTGTGTACCTGCTCTGC 156  
|||||

QY 2180 CACTGTATGTGGCATCTGTTATGCTAAAGTTTCTTGTACATAAACCCTCGGAAGACC 2239  
|||||  
DB 157 CACTGTATGTGGCATCTGTTATGCTAAAGTTTCTTGTACATAAACCCTCGGAAGACC 216  
|||||

QY 2240 TACTACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAATCTATTTGTGCTTTTAAT 2299  
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DB 217 TACTACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAATCTATTTGTGCTTTTAAT 276  
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QY 2300 AGAAGACAAATCCACC 2316  
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DB 277 AGAAGACAAATCCACC 293  
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RESULT 12  
BM455587  
LOCUS 1177 bp mRNA linear EST 05-FEB-2002  
DEFINITION AGENCOURT\_6407216 NIH\_MGC\_85 Homo sapiens cDNA clone IMAGE:5500647  
5', mRNA sequence.  
ACCESSION BM455587  
VERSION BM455587.1 GI:18504627  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1177)  
REFERENCE  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
MEDLINE Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Lou Staudt  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)



DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAMI2135 row: 0 column: 16

High quality sequence stop: 524.  
 Location/Qualifiers

FEATURES  
 source

1. .1177  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="5500647"  
 /clone\_lib="NIH\_MGC\_85"  
 /tissue\_type="lymphoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: lymph; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dr primed.  
 Average insert size 1.867 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."  
 434 a 208 c 343 g 191 t 1 others

BASE COUNT 434 a 208 c 343 g 191 t 1 others  
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 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db |  
 QY 186 CCCAGCTCATTTCTCTGGAAAGAGTTATTACCGATCCACATGTCCAGAGCACACA 245  
 Db |  
 QY 162 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGACAGCC 221  
 Db |  
 QY 246 GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGACAGCC 305  
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 QY 222 TATATGTTGAGTTCAGTCCAGTTCGACTTGTGATGAGCATCAGAGATGGTGC 281  
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 QY 306 TATATGTTGAGTTCAGTCCAGTTCGACTTGTGATGAGCATCAGAGATGGTGC 365  
 Db |  
 QY 282 GACAAACAGATGTAGATGAGTTCGACTTGTGATGAGCATCAGAGATGGTGC 341  
 Db |  
 QY 366 GACAAACAGATGTAGATGAGTTCGACTTGTGATGAGCATCAGAGATGGTGC 425  
 Db |  
 QY 342 CCCATGTGG 351  
 Db |  
 QY 426 CCCATGTGG 435

RESULT 13  
 BG698692  
 LOCUS  
 DEFINITION  
 602703045F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4800466 5',  
 mRNA sequence.  
 ACCESSION  
 BG698692  
 VERSION  
 BG698692.1 GI:13966211  
 KEYWORDS  
 EST.  
 SOURCE  
 human.  
 ORGANISM  
 Homo sapiens

REFERENCE  
 1 (bases 1 to 736)  
 AUTHORS  
 NIH-MGC  
 TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 Unpublished (1999)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAMI0691 row: 1 column: 11

High quality sequence stop: 733.  
 Location/Qualifiers

source

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 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 154 a 195 c 190 g 197 t

BASE COUNT 154 a 195 c 190 g 197 t  
 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 8e-104;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1377 TCTCTTTTTCAGCTTCTCAGGATGAGCTTTGGAGCCCGGAGAGAACTCCAAACA 1436  
 Db |  
 QY 104 TCTCTTTTTCAGCTTCTCAGGATGAGCTTTGGAGCCCGGAGAGAACTCCAAACA 163  
 Db |  
 QY 1437 ATCTGAGCTTCTCTTTAGACATTTCCAAAGCCCGGAGAGAACTCCAAACA 1496  
 Db |  
 QY 164 ATCTGAGCTTCTCTTTAGACATTTCCAAAGCCCGGAGAGAACTCCAAACA 223  
 Db |  
 QY 1497 TATCTCTATATTTTAAAGTGTGTGTTGATTTCCATGATATGTAGTGTGTGTG 1556  
 Db |  
 QY 224 TATCTCTATATTTTAAAGTGTGTGTTGATTTCCATGATATGTAGTGTGTGTG 283  
 Db |  
 QY 1557 TGTATGTGTGCGGTGTATCTAGCCCTCAAAACAGAGCTTGAAGACACTT 1609  
 Db |  
 QY 284 TGTATGTGTGCGGTGTATCTAGCCCTCAAAACAGAGCTTGAAGACACTT 336

RESULT 14

AW379300

LOCUS

DEFINITION

AW379300

VERSION

AW379300.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 565)

AUTHORS

HCGP

TITLE

The FAPESP/LICR Human Cancer Genome Project

JOURNAL

Unpublished (1999)

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-HT041-101299-003-a05&t3=1999-12-10&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 52

High quality sequence stop: 331.

Location/Qualifiers

1. .565

/organism="Homo sapiens"

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/clone\_lib="HT041"

/dev\_stage="Adult"

/note="Organ: head\_neck; Vector: puc18; Site\_1: SmaI;



Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.5e-102;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 956 GCAGTTGTTGGAGGATGAACCGCGTCAATTTTAATCATTTTACTCTGGAACCA 1015
Db 41 GCAGTTGTTGGAGGATGAACCGCGTCAATTTTAATCATTTTACTCTGGAACCA 100
QY 1016 GAGATGGCAAGTCCTGGGCGGACGCTGCTTTGAGGCCCGGATCTGTCTTGGCCAGAA 1075
Db 101 GAGATGGCAAGTCCTGGGCGGACGCTGCTTTGAGGCCCGGATCTGTCTTGGCCAGAA 160
QY 1076 GAGACAGAGCGCGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTACAAGA 1135
Db 161 GAGACAGAGCGCGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTACAAGA 220
QY 1136 ACGGTGATGTACCAAGCGCCGTTTCGTCAAGACACACATGGTATCCAG 1185
Db 221 ACGGTGATGTACCAAGCGCCGTTTCGTCAAGACACACATGGTATCCAG 270
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RESULT 15
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DEFINITION MRO-HT0241-091299-004-b02 HT0241 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW379296
VERSION    AW379296.1 GI:6883955
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 508)
            HGCP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0st2-MR0-HT0241-
            091299-004-b02st3-1999-12-09st4-1)
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            High quality sequence start: 72
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            Location/Qualifiers
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                    Site 2: SmaI; A mini-library was made by cloning products
                    derived from ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 - Ludwig Institute for Cancer Research)
                    profiles into the pUC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
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Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1114 CAAGTTTCGGACAGTACAAAGAACGGTGATGTACGAAGCCCGCTTTTCGTCAAGACACA 1173
Db 218 CAAGTTTCGGACAGTACAAAGAACGGTGATGTACGAAGCCCGCTTTTCGTCAAGACACA 277
QY 1174 CATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAAGTGTATATAC 1233
Db 278 CATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAAGTGTATATAC 337
QY 1234 TTACCAAGTGGGGCCCGTGAGACTTATGAATGCTGTGAAGATCAAGAGTCCCTCGAA 1293
Db 338 TTACCAAGTGGGGCCCGTGAGACTTATGAATGCTGTGAAGATCAAGAGTCCCTCGAA 397
QY 1294 CTCAATGCAGTACCTTCTCTCAGCACACAATTTGAAAACGTACAGGC 1336
Db 398 CTCAATGCAGTACCTTCTCTCAGCACACAATTTGAAAACGTACAGGC 440
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Search completed: June 28, 2003, 11:07:46  
Job time : 3506 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 07:30:13 ; Search time 601 Seconds  
(without alignments)  
10551.792 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2816	100.0	2816	AAZ25770	Human p51 encoding
2	2816	100.0	2816	AAC66029	Human lung cancer-
3	2816	100.0	2816	AAF86588	Human gene #1 used
4	2816	100.0	2816	ABL49248	Human p53 homology
5	1376	48.9	2270	AAZ25771	Human p51 encoding
6	1376	48.9	2270	AAC66028	Human lung cancer-
7	1376	48.9	2270	AAF86589	Human gene #2 used
8	1376	48.9	2270	ABL49247	Human p53 homology
9	1296	46.0	1347	AAZ58574	Human cell regulat

10	1275	45.3	4846	21	AAZ43913	Human KET CDNA. H
11	1275	45.3	4849	21	ABL66031	Human lung cancer-
12	1275	45.3	4849	24	ABL49250	Human p53 homology
13	1232	43.8	1551	20	AAZ58573	Human cell regulat
14	1232	43.8	1551	21	AAC66033	Human lung cancer-
15	1232	43.8	1551	24	ABL49252	Human p53 homology
16	1232	43.8	1926	20	AAZ58572	Human cell regulat
17	1141	40.5	1182	20	AAZ58576	Human cell regulat
18	1026	36.4	1386	21	AAC66032	Human p53 cancer-
19	1026	36.4	1386	24	ABL49251	Human p53 homology
20	1026	36.4	1761	20	AAZ58575	Human cell regulat
21	975	34.6	2082	20	AAZ27674	Human p40 coding s
22	975	34.6	2082	21	AAC66030	Human lung cancer-
23	975	34.6	2082	24	ABL49249	Human p53 homology
24	826	29.3	4655	21	AAC65887	Human lung cancer-
25	826	29.3	4655	24	ABL49106	Human lung tumour
26	822	29.2	2820	21	AAC66027	Human lung cancer-
27	822	29.2	2820	24	ABL49246	Human p53 homology
28	429	15.2	4643	20	AAZ24648	Human lung tumor a
29	308	10.9	308	22	AAF25912	Human tumor suppre
30	101	3.6	221	21	AAC17039	Human secreted pro
31	91	3.2	275	21	AAC17179	Human tumor suppre
32	90	3.2	5960	22	AAF25905	Human secreted pro
33	86	3.1	1452	20	AAZ58580	Mouse cell regulat
34	86	3.1	2043	20	AAZ58577	Human cell regulat
35	72	2.6	1170	20	AAZ58583	Mouse cell regulat
36	72	2.6	1386	20	AAZ58582	Mouse cell regulat
37	72	2.6	1761	20	AAZ58581	Mouse cell regulat
38	60	2.1	60	24	ABN40503	Human spliced tran
39	60	2.1	60	24	ABN58585	Human spliced tran
40	60	2.1	60	24	ABN58586	Human spliced tran
41	60	2.1	60	24	ABN58587	Human spliced tran
42	60	2.1	60	24	ABN58843	Human spliced tran
43	45	1.6	4708	21	AAZ43912	Rat KET CDNA. Rat
44	30	1.1	346	22	AAZ58883	Human polynucleoti
45	30	1.1	4365	21	AAA29172	Human vanilloid re

ALIGNMENTS

RESULT 1

AAZ25770

ID AAZ25770 standard; cDNA; 2816 BP.

AC AAZ25770;

XX 07-JAN-2000 (first entry)

DE Human p51 encoding cDNA A.

XX Human; p51; p53 related gene; cell proliferation; regulation; cancer;

KW tumour suppression; diagnosis; ss.

XX Homo sapiens.

OS Key

FT CDS

FT polyA\_signal

FT FT

XX WO9950412-A1.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-JP01512.

XX 27-MAR-1998; 98JP-0100467.

XX (SAKA ) OTSUKA PHARM CO LTD.

XX (IKAWA) IKAWA Y.

XX

PI Ikawa Y, Ikawa S, Obinata M;  
XX WPI; 1999-591318/50.  
DR P-PSDB; AAY45246.  
XX  
PT New p53 related human gene p51, useful for diagnosis, investigation and  
PT treatment of cancers and screening for potential cell proliferation  
PT agents -  
XX  
XX  
PS Claim 3; Page 148-151; 163pp; Japanese.  
XX  
XX The present sequence represents a human p51 gene, which is related to  
CC p53 and has cell proliferation regulation and tumour suppression  
CC activity. The p51 gene can be used in the investigation, diagnosis and  
CC treatment of diseases such as cancer, with which the p53 family cell  
CC proliferation regulation is associated. The p51 protein may be used for  
CC screening potential agonists and antagonists of its regulatory function,  
CC for use as drugs,  
XX  
SQ Sequence 2816 BP; 781 A; 658 C; 619 G; 758 T; 0 other;  
  
Query Match 100.0%; Score 2816; DB 20; Length 2816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 TCGTTGATATCAAGACAGTTGAAGAAATGAATTTGAAACTTCACGGTGTGCCACCT 60  
  
QY 61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTCGTAGAACCAGCTCATTTCTCTGG 120  
DB 61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTCGTAGAACCAGCTCATTTCTCTGG 120  
  
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QY 181 CCAGAGGTTTCCAGCATATCTGGATTTCTGGAACAGCCTATATGTTTCAGTTCAGCCC 240  
DB 181 CCAGAGGTTTCCAGCATATCTGGATTTCTGGAACAGCCTATATGTTTCAGTTCAGCCC 240  
  
QY 241 ATTGACTTGAACCTTTGATGAACCATCAGAAAGATGGTGGCAACAAAGATTGAGATT 300  
DB 241 ATTGACTTGAACCTTTGATGAACCATCAGAAAGATGGTGGCAACAAAGATTGAGATT 300  
  
QY 301 AGCATGGACTATCCGCATGCGAGACTCGGACCTGAGTGACCCCATGCGGCACAGTAC 360  
DB 301 AGCATGGACTATCCGCATGCGAGACTCGGACCTGAGTGACCCCATGCGGCACAGTAC 360  
  
QY 361 ACAGAACTGGGGCTCTGAAACAGCATGGACAGCAGATTGAGAGCGCTCCCTCGTCCACC 420  
DB 361 ACAGAACTGGGGCTCTGAAACAGCATGGACAGCAGATTGAGAGCGCTCCCTCGTCCACC 420  
  
QY 421 AGTCCCTATTAACACAGACACCGGAGAACAGCGTCAAGCGCCCTCGCCCTACGCACAG 480  
DB 421 AGTCCCTATTAACACAGACACCGGAGAACAGCGTCAAGCGCCCTCGCCCTACGCACAG 480  
  
QY 481 CCAGCTCCACCTTCGATGCTCTCTCCATCAGCGCCATCCCTCCAGACAGCTAC 540  
DB 481 CCAGCTCCACCTTCGATGCTCTCTCCATCAGCGCCATCCCTCCAGACAGCTAC 540  
  
QY 541 CCAGGCCCCGACAGTTTCGACGTGCTCTTCCAGCAGTCGAGCAGCGCCCAAGTCGGCCACC 600  
DB 541 CCAGGCCCCGACAGTTTCGACGTGCTCTTCCAGCAGTCGAGCAGCGCCCAAGTCGGCCACC 600  
  
QY 601 TGGACGTATTCACCTGAACCTGAAGAACTCTACTGCCAAATGGAAGACATGCCCATC 660  
DB 601 TGGACGTATTCACCTGAACCTGAAGAACTCTACTGCCAAATGGAAGACATGCCCATC 660  
  
QY 661 CAGATCAAGGTGATGACCCCACTCTCAGGAGCTGTTATCCGCGCCATGCTCTCTAC 720  
DB 661 CAGATCAAGGTGATGACCCCACTCTCAGGAGCTGTTATCCGCGCCATGCTCTCTAC 720

QY 721 AAAAAAGCTGAGCAGCTACGAGGTTGGTGAAGCGGTGCCCCAACCAATGAGCTGAGCCGT 780  
DB 721 AAAAAAGCTGAGCAGCTACGAGGTTGGTGAAGCGGTGCCCCAACCAATGAGCTGAGCCGT 780  
  
QY 781 GAATTTCAACGAGGACAGATTGCCCTCCCTAGTTCATTTGATTGAGTGGAGGGAACAGC 840  
DB 781 GAATTTCAACGAGGACAGATTGCCCTCCCTAGTTCATTTGATTGAGTGGAGGGAACAGC 840  
  
QY 841 CATGCCAGTATGTAGAAAGATCCATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAG 900  
DB 841 CATGCCAGTATGTAGAAAGATCCATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAG 900  
  
QY 901 CCACCCAGGTTGGCACTGAATTCAGACAGCTCTGTACAAATTTTCATGTTAAACAGAGT 960  
DB 901 CCACCCAGGTTGGCACTGAATTCAGACAGCTCTGTACAAATTTTCATGTTAAACAGAGT 960  
  
QY 961 TGTGTTGGAGGATGAACCCCGCTCCAAATTTTAACTTCTTACTCTGGAACACAGAGAT 1020  
DB 961 TGTGTTGGAGGATGAACCCCGCTCCAAATTTTAACTTCTTACTCTGGAACACAGAGAT 1020  
  
QY 1021 GGCAAGTCTTGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGGCCAGGAAGAGAC 1080  
DB 1021 GGCAAGTCTTGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGGCCAGGAAGAGAC 1080  
  
QY 1081 AGGAAGCGGATGAAGATAGCATGAGAAAGACAGCAAGTTTCGACAGTACAAAGACGCT 1140  
DB 1081 AGGAAGCGGATGAAGATAGCATGAGAAAGACAGCAAGTTTCGACAGTACAAAGACGCT 1140  
  
QY 1141 GATGTTACGAAGCGCCGCTTTCGTGAGAACACACATGATCCAGATGATGAGGCGCTGAGACTTAT 1200  
DB 1141 GATGTTACGAAGCGCCGCTTTCGTGAGAACACACATGATCCAGATGATGAGGCGCTGAGACTTAT 1200  
  
QY 1201 AAACGAAGATCCCGAGATGATGAATGTTTATCTTACAGTACGAGGCGCTGAGACTTAT 1260  
DB 1201 AAACGAAGATCCCGAGATGATGAATGTTTATCTTACAGTACGAGGCGCTGAGACTTAT 1260  
  
QY 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGAGTACCTTCTCAGACACACA 1320  
DB 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGAGTACCTTCTCAGACACACA 1320  
  
QY 1321 ATTGAACCTTACGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380  
DB 1321 ATTGAACCTTACGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380  
  
QY 1381 CTTTCAGCTGCTTTCAGGAATCAGCTTGTGGAGCCCCGAGAGAACTCCAAACAACT 1440  
DB 1381 CTTTCAGCTGCTTTCAGGAATCAGCTTGTGGAGCCCCGAGAGAACTCCAAACAACT 1440  
  
QY 1441 GACGTCTTCTTAGACATTCAGCCCTCAAAACCGATCAGTGTACCCATAGAGCCCTATC 1500  
DB 1441 GACGTCTTCTTAGACATTCAGCCCTCAAAACCGATCAGTGTACCCATAGAGCCCTATC 1500  
  
QY 1501 TCTATATTTAAGTCTGTGTGTTGATTTCCATGATATGATGATGATGATGATGATGATGAT 1560  
DB 1501 TCTATATTTAAGTCTGTGTGTTGATTTCCATGATATGATGATGATGATGATGATGATGAT 1560  
  
QY 1561 TGTGTTGGTGTGTGTATAGCCCTCAAAACCGATCAGTGTGATGATGATGATGATGATGATGAT 1620  
DB 1561 TGTGTTGGTGTGTGTATAGCCCTCAAAACCGATCAGTGTGATGATGATGATGATGATGATGAT 1620  
  
QY 1621 CCCAACTGCTCAAAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1680  
DB 1621 CCCAACTGCTCAAAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1680  
  
QY 1681 TTACAAGAAAGATGTTTCTGCAAGATTTTCTATCTTACCTTAGACCGGCAATGCTGGGTGAG 1740  
DB 1681 TTACAAGAAAGATGTTTCTGCAAGATTTTCTATCTTACCTTAGACCGGCAATGCTGGGTGAG 1740  
  
QY 1741 GAACCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800  
DB 1741 GAACCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800  
  
QY 1801 GAAAGGGCATTAAAGATGTTTATTTGGAACCCCTTTTCTGCTCTTCTGTTGTTTCTTAA 1860

1801 GAAAGGCGCATTAAGATGTTTATTGGAACCCCTTTCTGCTCTCTCTGTTGTTCTTCTAA 1860  
1861 AATTACAGGGAAGCTTTGAGCAGGCTCTAAACCTTAAGATGCTTTTAAAGAAAGGAG 1920  
1861 AATTACAGGGAAGCTTTGAGCAGGCTCTAAACCTTAAGATGCTTTTAAAGAAAGGAG 1920  
1921 AAAAAGTTGTTATTGCTGTGCATTAAGTAAGTGTAGGTGACTGAGAGACTCAGTCAGA 1980  
1921 AAAAAGTTGTTATTGCTGTGCATTAAGTAAGTGTAGGTGACTGAGAGACTCAGTCAGA 1980  
1981 CCCTTTTAAGCTGGTCATGTAATAATTAATGCAAGTAGTAAGAAACGAAGGTGCAAGTG 2040  
1981 CCCTTTTAAGCTGGTCATGTAATAATTAATGCAAGTAGTAAGAAACGAAGGTGCAAGTG 2040  
2041 TACTGCTGGCAGCGAGGTGATCAATACCAAACTAATCACTTTGGTGGGAGAGTTC 2100  
2041 TACTGCTGGCAGCGAGGTGATCAATACCAAACTAATCACTTTGGTGGGAGAGAGTTC 2100  
2101 TTTGTGAGAACTTGCATTATTGTCCTCCCTCATGCTGTAGTAGAACAATTTCTTAAT 2160  
2101 TTTGTGAGAACTTGCATTATTGTCCTCCCTCATGCTGTAGTAGAACAATTTCTTAAT 2160  
2161 GCTGTGACCTGCTGCGCACTGTATGTTGGCACTGTTATGCTAAAGTTTCTTGTGA 2220  
2161 GCTGTGACCTGCTGCGCACTGTATGTTGGCACTGTTATGCTAAAGTTTCTTGTGA 2220  
2221 CATGAACCCCTGGAGACCTACTACAAAACCTGTTGTTGGCCCCCATAGCAGGTGAA 2280  
2221 CATGAACCCCTGGAGACCTACTACAAAACCTGTTGTTGGCCCCCATAGCAGGTGAA 2280  
2281 CTCAATTTGCTGTTTAAAGAAACAAATCCACCCAGTAATATTGCCCTTACGTAGT 2340  
2281 CTCAATTTGCTGTTTAAAGAAACAAATCCACCCAGTAATATTGCCCTTACGTAGT 2340  
2341 TGTTTACCATTTTCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400  
2341 TGTTTACCATTTTCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400  
2401 AATTGCTTAAATAGAGCTCTATCCCTCAAGCCTACCTACCATAAAACAGCCATATTA 2460  
2401 AATTGCTTAAATAGAGCTCTATCCCTCAAGCCTACCTACCATAAAACAGCCATATTA 2460  
2461 CTGATCTGTTCACTGATTTAGCCAGGAGACTTTACGTTTGTAGTAAAGTCCCAAGC 2520  
2461 CTGATCTGTTCACTGATTTAGCCAGGAGACTTTACGTTTGTAGTAAAGTCCCAAGC 2520  
2521 AGACGTGTTAAATCAGCAGCTCCCTGGACTGGAAATTAAGATTGAAAGGTAGACTACTT 2580  
2521 AGACGTGTTAAATCAGCAGCTCCCTGGACTGGAAATTAAGATTGAAAGGTAGACTACTT 2580  
2581 TTCTTTTACCTCAAAAGTTTAAAGATCTCTGTTCTTCCATTTTAAACATATT 2640  
2581 TTCTTTTACCTCAAAAGTTTAAAGATCTCTGTTCTTCCATTTTAAACATATT 2640  
2641 TTAAGATAAATAGCATAAGACTTTTAAAGATCTCTGTTCTTCCATTTTAAACATATT 2700  
2641 TTAAGATAAATAGCATAAGACTTTTAAAGATCTCTGTTCTTCCATTTTAAACATATT 2700  
2701 CACGAGCAGCTGATTTTCTGTACCAAGACAAATGATTCTTGTGTTATTGAGGCTGTGCTT 2760  
2701 CACGAGCAGCTGATTTTCTGTACCAAGACAAATGATTCTTGTGTTATTGAGGCTGTGCTT 2760  
2761 TTGTGGATGTGATTTTAAATTTCAATAAACTTTTGCATCTTGGTTTAAAGAAA 2816  
2761 TTGTGGATGTGATTTTAAATTTCAATAAACTTTTGCATCTTGGTTTAAAGAAA 2816

RESULT 2  
AAC66029  
ID AAC66029 standard; cDNA; 2816 BP.  
XX  
AC AAC66029;

XX 21-FEB-2001 (first entry)  
DT Human lung cancer-associated cDNA p63 isoform 3.  
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
XX vaccine; detection; ss.  
XX Homo sapiens.  
OS  
XX WO2000061612-A2.  
FN 19-OCT-2000.  
XX  
XX 03-APR-2000; 2000WO-US08896.  
XX 02-APR-1999; 99US-0285479.  
PR 17-DEC-1999; 99US-0466396.  
PR 30-DEC-1999; 99US-0476496.  
PR 10-JAN-2000; 2000US-0480884.  
PR 22-FEB-2000; 2000US-0510376.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Fan L;  
XX  
XX WPI: 2000-628399/60.  
XX P-PSDB; AAB11359.  
XX  
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor  
XX protein is used for detecting and monitoring progression of lung cancer  
XX in a patient -  
XX  
XX Claim 25a; Page 238-239; 261pp; English.  
XX  
XX This invention describes a novel isolated polypeptide (I) which  
XX comprising an immunogenic portion of a lung tumor protein or variant (P2)  
XX which have cytostatic activity. The polypeptides and polynucleotides are  
XX used in compositions and vaccines to inhibit the development of cancer.  
XX especially lung cancer, in a patient. Methods described in the invention  
XX can be used to monitor the progression of a cancer by carrying out the  
XX detection at subsequent time points and comparing the results from the  
XX different time points. CD4+ and/or CD8+ T-Cells isolated from a patient  
XX are treated with P2, polynucleotides encoding P2 or antigen presenting  
XX cells expressing P2 and then administered to the patient to inhibit  
XX development of cancer.

Sequence 2816 BP; 781 A; 658 C; 619 G; 758 T; 0 other;  
Query Match 100.0%; Score 2816; DB 21; Length 2816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCGTTGATATCAAAAGACAGAGTTGAAGGAAATGAATTTTGAACCTTACCGTGTGCCACCT 60  
DB 1 TCGTTGATATCAAAAGACAGAGTTGAAGGAAATGAATTTTGAACCTTACCGTGTGCCACCT 60  
QY 61 ACAGTACTGCCCTGACCCCTTACATCCAGCTTTCGTAGAAACCCAGCTCATTTCTTTGG 120  
DB 61 ACAGTACTGCCCTGACCCCTTACATCCAGCTTTCGTAGAAACCCAGCTCATTTCTTTGG 120  
QY 121 AAAGAAAGTTATTACCGATCCACCATGTCGCCAGAGCACACAGACAAATGAATTCCTCAGT 180  
DB 121 AAAGAAAGTTATTACCGATCCACCATGTCGCCAGAGCACACAGACAAATGAATTCCTCAGT 180  
QY 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTTCTAGTTCAGCCC 240  
DB 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTTCTAGTTCAGCCC 240  
QY 241 ATTGACTTGAACCTTTTGTGGATGAACCATCATCAGAAGATGTGGACAAACAGATGAGATT 300  
DB 241 ATTGACTTGAACCTTTTGTGGATGAACCATCATCAGAAGATGTGGACAAACAGATGAGATT 300

QY	301	AGCATGGACTGTATCCGATGCGAGCTCGGACCTGAGTGACCCCATCTGTGGCCACAGTAC	360		1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACAACTCT	1440
Db	301	AGCATGGACTGTATCCGATGCGAGCTCGGACCTGAGTGACCCCATCTGTGGCCACAGTAC	360				
QY	361	ACGAACCTGGGGCTCCTGAACAGCATGACAGCATGACAGATTCAGAACGGCTCCTGTCACAC	420		1441	GAGCTCTCTTTAGACATTCCAAGAGCCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC	1500
Db	361	ACGAACCTGGGGCTCCTGAACAGCATGACAGCATGACAGATTCAGAACGGCTCCTGTCACAC	420		1441	GAGCTCTCTTTAGACATTCCAAGAGCCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC	1500
QY	421	AGTCCCTATTAACACAGACACCGGCGAGAACAGGCTCACGGCGCCCTCGCCCTACGCACAG	480		1501	TCATATTTTAAAGTGTGTGTATTTCCATGTCTATATGTAGTGTGTGTGTGTGTGTGTGT	1560
Db	421	AGTCCCTATTAACACAGACACCGGCGAGAACAGGCTCACGGCGCCCTCGCCCTACGCACAG	480		1501	TCATATTTTAAAGTGTGTGTATTTCCATGTCTATATGTAGTGTGTGTGTGTGTGTGTGT	1560
QY	481	CCGAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCAAACACCGACTAC	540		1561	TGTGTGGCTGTGTATCTAGCCCTCATAAACAGAGACTTGAAGACACTTTGGCTCAGAGA	1620
Db	481	CCGAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCAAACACCGACTAC	540		1561	TGTGTGGCTGTGTATCTAGCCCTCATAAACAGAGACTTGAAGACACTTTGGCTCAGAGA	1620
QY	541	CCAGGCCCGCACAGTTTCGAGCTGCTCTCCAGCAGTCGAGCAGCCGCAAGTCGGCCACC	600		1621	CCCAACTGCTCAAAAGCACAAGCCACTAGTGAGAGAACTCTTTGAAGGAGCTCAAACT	1680
Db	541	CCAGGCCCGCACAGTTTCGAGCTGCTCTCCAGCAGTCGAGCAGCCGCAAGTCGGCCACC	600		1621	CCCAACTGCTCAAAAGCACAAGCCACTAGTGAGAGAACTCTTTGAAGGAGCTCAAACT	1680
QY	601	TGGACGTATTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGAAGACATGCCCATC	660		1681	TTACAAAGAAAGATGTTTCTGCAGATTTGTATCTTACCGGCCATTGTTGGGTGAG	1740
Db	601	TGGACGTATTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGAAGACATGCCCATC	660		1681	TTACAAAGAAAGATGTTTCTGCAGATTTGTATCTTACCGGCCATTGTTGGGTGAG	1740
QY	661	CAGATCAAGTGTATGACCCACCTCCTCAGGAGCTGTTATCCGCGCCATGCCGTGTAC	720		1741	GAACCACTGTGTTCTGTGAGCTTCTGTTGTTTCTCTGCTCTCTCTCTCTCTCTCTCT	1800
Db	661	CAGATCAAGTGTATGACCCACCTCCTCAGGAGCTGTTATCCGCGCCATGCCGTGTAC	720		1741	GAACCACTGTGTTCTGTGAGCTTCTGTTGTTTCTCTGCTCTCTCTCTCTCTCTCTCT	1800
QY	721	AAAAAGCTGAGCAGCTGACGGAGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCGT	780		1801	GAAAGGGGCAATTAAGATGTTTGAACCCCTTTCTGCTCTCTCTCTCTCTCTCTCTCT	1860
Db	721	AAAAAGCTGAGCAGCTGACGGAGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCGT	780		1801	GAAAGGGGCAATTAAGATGTTTGAACCCCTTTCTGCTCTCTCTCTCTCTCTCTCTCT	1860
QY	781	GAATTCACGAGGACAGATGCCCCCTCTAGTCAATTTGATTCGAGTACGAGGGAACAGC	840		1861	AATTCACAGGAGGCTTTTGGAGGCTCTCAAACTTAAGATGCTCTTTTAAAGAAAGAG	1920
Db	781	GAATTCACGAGGACAGATGCCCCCTCTAGTCAATTTGATTCGAGTACGAGGGAACAGC	840		1861	AATTCACAGGAGGCTTTTGGAGGCTCTCAAACTTAAGATGCTCTTTTAAAGAAAGAG	1920
QY	841	CATGCCAGTATGTAGAAGATCCATCAGAGGAGACAGTGTCTGCTGCTGCTGCTGCTG	900		1921	AAAAAGTTGTTATTGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1980
Db	841	CATGCCAGTATGTAGAAGATCCATCAGAGGAGACAGTGTCTGCTGCTGCTGCTGCTG	900		1921	AAAAAGTTGTTATTGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1980
QY	901	CCACCCAGGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960		1981	CCCTTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2040
Db	901	CCACCCAGGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960		1981	CCCTTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2040
QY	961	TGTGTTGGAGGATGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020		2041	TACTGCTGGCAGCAGGCTGATCATTAACAAAGTAACTAAGTGTGGGTGGAGGTTTC	2100
Db	961	TGTGTTGGAGGATGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020		2041	TACTGCTGGCAGCAGGCTGATCATTAACAAAGTAACTAAGTGTGGGTGGAGGTTTC	2100
QY	1021	GGCAAGTCTTGGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080		2101	TTTGTGAGAACTTGCATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2160
Db	1021	GGCAAGTCTTGGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080		2101	TTTGTGAGAACTTGCATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2160
QY	1081	AGGAAGCGGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1140		2161	GCTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2220
Db	1081	AGGAAGCGGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1140		2161	GCTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2220
QY	1141	GATGTGACGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200		2221	CATGAAACCTCGGAAGACCTTACTACAAAAGTAACTGTTTGGGCCCCCATAGAGTGA	2280
Db	1141	GATGTGACGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200		2221	CATGAAACCTCGGAAGACCTTACTACAAAAGTAACTGTTTGGGCCCCCATAGAGTGA	2280
QY	1201	AAACGAAGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1260		2281	CTCATTTTGTGCTTTTAAATAGAACACAAATCCACCCAGTAAATATGCTGCTGCTG	2340
Db	1201	AAACGAAGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1260		2281	CTCATTTTGTGCTTTTAAATAGAACACAAATCCACCCAGTAAATATGCTGCTGCTG	2340
QY	1261	GAATGCTGTTGAAGATCAAGAGTCCCTGGAACATGATGATGATGATGATGATGAT	1320		2341	TGTTTACCATTATTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTG	2400
Db	1261	GAATGCTGTTGAAGATCAAGAGTCCCTGGAACATGATGATGATGATGATGATGAT	1320		2341	TGTTTACCATTATTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTG	2400
QY	1321	ATTGAAACCTACAGGACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1380		2401	AATTTGCTTATTTAGAGCTTCTATCCCTCAAGCCTTACCTACCAATAAAACAGGCA	2460
Db	1321	ATTGAAACCTACAGGACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1380		2401	AATTTGCTTATTTAGAGCTTCTATCCCTCAAGCCTTACCTACCAATAAAACAGGCA	2460
QY	1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACAACT	1440		2461	CTGATCTGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT	2520
Db	1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACAACT	1440		2461	CTGATCTGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT	2520







```
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
DR P-PSDB; ABB74991.
DR
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
PT
XX Example 2; Page 315-316; 374pp; English.
PS
XX The present invention describes human lung tumour proteins. Human lung
XX tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
CC ABB75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 2816 BP; 781 A; 658 C; 619 G; 758 T; 0 other;
SQ
Query Match 100.0%; Score 2816; DB 24; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTTGATATCAAGACAGTTGAAGAAATGAAATTTGAACTTCACGGTGTGCCACCT 60
DB 1 TCGTTGATATCAAGACAGTTGAAGAAATGAAATTTGAACTTCACGGTGTGCCACCT 60
QY 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCAFTTCTCTGG 120
DB 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCAFTTCTCTGG 120
QY 121 AAAGAAAGTATTACCATCCACCATGTCCAGAGCACACAGAAATGAATTCCTCAGT 180
DB 121 AAAGAAAGTATTACCATCCACCATGTCCAGAGCACACAGAAATGAATTCCTCAGT 180
QY 181 CCAGAGGTTTCCAGCATATCTGGATTTCTGGAACAGCCTATATGTTTCAGTTTCAGGCC 240
DB 181 CCAGAGGTTTCCAGCATATCTGGATTTCTGGAACAGCCTATATGTTTCAGTTTCAGGCC 240
QY 241 ATTGACTTGAATTTGTTGGATGAACCATCAAGAGATGGTGGCAGAAACAAAGATTGAGATT 300
DB 241 ATTGACTTGAATTTGTTGGATGAACCATCAAGAGATGGTGGCAGAAACAAAGATTGAGATT 300
QY 301 AGCATGACTGTATCCGATGTCAGACTCGACCTGAGTGCACCCATGTGCCACAGTAC 360
DB 301 AGCATGACTGTATCCGATGTCAGACTCGACCTGAGTGCACCCATGTGCCACAGTAC 360
QY 361 ACAGAACTGGGGCTCTGAAACAGCATGGACAGAGATTCAGAACGGCTCTCTGTCAC 420
DB 361 ACAGAACTGGGGCTCTGAAACAGCATGGACAGAGATTCAGAACGGCTCTCTGTCAC 420
QY 421 AGTCCCTATACACAGACCCAGCGCAGAACAGCTGCAGCGCCCTCGCCCTAGCCACAG 480
DB 421 AGTCCCTATACACAGACCCAGCGCAGAACAGCTGCAGCGCCCTCGCCCTAGCCACAG 480
QY 481 CCCAGCTCCAGCTTCGATGCTCTCTCCATFACCCCGCCATCCCTCCAAACACGACTAC 540
DB 481 CCCAGCTCCAGCTTCGATGCTCTCTCCATFACCCCGCCATCCCTCCAAACACGACTAC 540
QY 541 CCAGGCCCGCACATTTCCAGCTGTCTTCCAGCAGTCGAGCACCAGCCGCAAGTCGGCCACC 600
DB 541 CCAGGCCCGCACATTTCCAGCTGTCTTCCAGCAGTCGAGCACCAGCCGCAAGTCGGCCACC 600
QY 601 TGGACGTATTCCTCACTGAAGAACTCTACTGCCAAATTCGAAAGACATGCCCCATC 660
DB 601 TGGACGTATTCCTCACTGAAGAACTCTACTGCCAAATTCGAAAGACATGCCCCATC 660
QY 661 CAGATCAAGGTGATGACCCCTCTCAGGAGCTGTTATCCGGCCCATGCTCTCTAC 720
DB 661 CAGATCAAGGTGATGACCCCTCTCAGGAGCTGTTATCCGGCCCATGCTCTCTAC 720
QY 721 AAAAAGCTGAGCAGCTCAGCGAGTGGTGAAGCGGTCCCAACCATGAGCTGAGCCGT 780
DB 721 AAAAAGCTGAGCAGCTCAGCGAGTGGTGAAGCGGTCCCAACCATGAGCTGAGCCGT 780
QY 781 GAATTCACAGGAGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGAACAGC 840
DB 781 GAATTCACAGGAGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGAACAGC 840
QY 841 CATGCCAGTATGTAGAAGATCCCATCACAGAGACAGAGTGTCTGCTACCTTATGAG 900
DB 841 CATGCCAGTATGTAGAAGATCCCATCACAGAGACAGAGTGTCTGCTGCTATGAG 900
QY 901 CCACCCAGGTTGGCAGCTGAATTCACGACAGCTTGTGTACAATTTTCATCTGTAAACAGCAGT 960
DB 901 CCACCCAGGTTGGCAGCTGAATTCACGACAGCTTGTGTACAATTTTCATCTGTAAACAGCAGT 960
QY 961 TGTGTTGAGGAGTGAACCGCGCTCAATTTTAATCATTTGTTACTCTCGAAACACAGAT 1020
DB 961 TGTGTTGAGGAGTGAACCGCGCTCAATTTTAATCATTTGTTACTCTCGAAACACAGAT 1020
QY 1021 GGGCAAGTCTGGGCCGAGCGTGTCTTGGGCCCGGATCTGTCTTGGCCAGGAGAGAC 1080
DB 1021 GGGCAAGTCTGGGCCGAGCGTGTCTTGGGCCCGGATCTGTCTTGGCCAGGAGAGAC 1080
QY 1081 AGGAAGCGGATGAAGATGATGATCAGAAGCAGCAAGTTTCGGACAGTACAAAGAACCGT 1140
DB 1081 AGGAAGCGGATGAAGATGATGATCAGAAGCAGCAAGTTTCGGACAGTACAAAGAACCGT 1140
QY 1141 GATGATAGGAAGCGCCCTTTTCGTAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
DB 1141 GATGATAGGAAGCGCCCTTTTCGTAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGATCCACAGATGATGAATCTTATCTTACCAGTCAGGGCGGTGAGACTTAT 1260
DB 1201 AAACGAAGATCCACAGATGATGAATCTTATCTTACCAGTCAGGGCGGTGAGACTTAT 1260
QY 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGACAGTACTTCTCTCAGCACACA 1320
DB 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGACAGTACTTCTCTCAGCACACA 1320
QY 1321 ATTGAAGCGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGTACTTACTTCAGAAACATCTC 1380
DB 1321 ATTGAAGCGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGTACTTACTTCAGAAACATCTC 1380
QY 1381 CTTTCAGCTCTCTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAACAAATCT 1440
DB 1381 CTTTCAGCTCTCTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAACAAATCT 1440
QY 1441 GAGCTCTCTTTTGAACATTTCAAGCCCAACACCGATCAGTGTACCCATAGAGCCCTATC 1500
DB 1441 GAGCTCTCTTTTGAACATTTCAAGCCCAACACCGATCAGTGTACCCATAGAGCCCTATC 1500
QY 1501 TCTATATTTTAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
DB 1501 TCTATATTTTAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
QY 1561 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
DB 1561 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 1621 CCCAACTGCTCAAAAGGCAAAAGCACTAGTGTAGAGAACTTTTCAAGGGGACTCAAACT 1680
DB 1621 CCCAACTGCTCAAAAGGCAAAAGCACTAGTGTAGAGAACTTTTCAAGGGGACTCAAACT 1680
QY 1681 TTACAAGAAAGGATGTTTTTCTGCAGATTTTGTATCTTCTTACCCGCGCCATTTGTTGGTGTGAG 1740
```

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Db 1681 TTAAGGAAAGGATGTTTCTGACAGATTTTGTATCTTAGACCGCCATTGGTGGGTGAG 1740
Qy 1741 GAACCACTGTGTTGTTCTGTGAGCTTCTGTGTTTCTCTGGAGGAGGGTCAAGTGGG 1800
Db 1741 GAACCACTGTGTTGTTCTGTGAGCTTCTGTGTTTCTCTGGAGGAGGGTCAAGTGGG 1800
Qy 1801 GAAAGGGCCATTAAGATGTTTATTTGGAACCTTTCTCTGTCTTCTGTTGTTTCTTAA 1860
Db 1801 GAAAGGGCCATTAAGATGTTTATTTGGAACCTTTCTCTGTCTTCTGTTGTTTCTTAA 1860
Qy 1861 AATTACAGGGAAGCTTTGAGCAGGCTCAAACTTAAGATGCTTTTAAAGAAAGGAG 1920
Db 1861 AATTACAGGGAAGCTTTGAGCAGGCTCAAACTTAAGATGCTTTTAAAGAAAGGAG 1920
Qy 1921 AAAAAAGTTGTTATTTCTGTGATAGTAAAGTGTAGTGACTGAGAGACTCAGTCAGA 1980
Db 1921 AAAAAAGTTGTTATTTCTGTGATAGTAAAGTGTAGTGACTGAGAGACTCAGTCAGA 1980
Qy 1981 CCCTTTTAAGCTGGTCAATGTAATATTTGCAAGTAGTAAAGAAAGGAGTCAAGTG 2040
Db 1981 CCCTTTTAAGCTGGTCAATGTAATATTTGCAAGTAGTAAAGAAAGGAGTCAAGTG 2040
Qy 2041 TACTGCTGGCAGGAGTCAATACCAAAAGTAACTAATCAACTTTGTGGGTGAGAGTTC 2100
Db 2041 TACTGCTGGCAGGAGTCAATACCAAAAGTAACTAATCAACTTTGTGGGTGAGAGTTC 2100
Qy 2101 TTTGTGAGAACTTGCATATTTGTGCTCCCTCATGTAGTAGTAAAGTCTTCTTAA 2160
Db 2101 TTTGTGAGAACTTGCATATTTGTGCTCCCTCATGTAGTAGTAAAGTCTTCTTAA 2160
Qy 2161 GCTGTGTACCTGCTGCGACATGTTGTCCTCCCTCATGTAGTAGTAAAGTCTTCTTAA 2220
Db 2161 GCTGTGTACCTGCTGCGACATGTTGTCCTCCCTCATGTAGTAGTAAAGTCTTCTTAA 2220
Qy 2221 CATGAAACCTCGAAGACCTTACTACAAAAGTCTGTTGTCCTCCCTCATGAGTAA 2280
Db 2221 CATGAAACCTCGAAGACCTTACTACAAAAGTCTGTTGTCCTCCCTCATGAGTAA 2280
Qy 2281 CTCAATTTGTGCTTTTAAAGAAAGCAATCCACCCAGTAAATATTTGCCCTTACGTAGT 2340
Db 2281 CTCAATTTGTGCTTTTAAAGAAAGCAATCCACCCAGTAAATATTTGCCCTTACGTAGT 2340
Qy 2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGAT 2400
Db 2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGAT 2400
Qy 2401 AATTGCTTAAATAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAACCCAGCATATTA 2460
Db 2401 AATTGCTTAAATAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAACCCAGCATATTA 2460
Qy 2461 CTGATACCTCTCAGTGCATTTAGCCAGGAGACTTACGTTTTCAGTAAGTGAATCCAAGC 2520
Db 2461 CTGATACCTCTCAGTGCATTTAGCCAGGAGACTTACGTTTTCAGTAAGTGAATCCAAGC 2520
Qy 2521 AGACGTGTTTAAATCAGCACTCCTGAGCTGGAATTAAGATTTGAAGGGTGAAGTACTT 2580
Db 2521 AGACGTGTTTAAATCAGCACTCCTGAGCTGGAATTAAGATTTGAAGGGTGAAGTACTT 2580
Qy 2581 TTCCTTTTAAATCAGCACTCCTGAGCTGGAATTAAGATTTGAAGGGTGAAGTACTT 2640
Db 2581 TTCCTTTTAAATCAGCACTCCTGAGCTGGAATTAAGATTTGAAGGGTGAAGTACTT 2640
Qy 2641 TTAAGATATACATTAAGACTTTTAAAGTGTCTCCCTCCATCTTCCACACCCAGT 2700
Db 2641 TTAAGATATACATTAAGACTTTTAAAGTGTCTCCCTCCATCTTCCACACCCAGT 2700
Qy 2701 CACCACTGCTGTTTCTGTCAACCAAGCAATGTTTCTGTTTATTTGAGGCTGTGCTT 2760
Db 2701 CACCACTGCTGTTTCTGTCAACCAAGCAATGTTTCTGTTTATTTGAGGCTGTGCTT 2760
Qy 2761 TTGTCGATGTGATTTTAAATTTCAATAACTTTTTCATCTGTGTTTAAAGAAA 2816
Db 2761 TTGTCGATGTGATTTTAAATTTCAATAACTTTTTCATCTGTGTTTAAAGAAA 2816
```

```
Db 2761 TTGTCGATGTGATTTTAAATTTCAATAACTTTTTCATCTGTGTTTAAAGAAA 2816
RESULT 5
AAZ25771
ID AAZ25771 standard; cDNA; 2270 BP.
XX
XX AAZ25771;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human p51 encoding cDNA B.
DE
XX Human; p51; p53 related gene; cell proliferation; regulation; cancer;
XX tumour suppression; diagnosis; ss.
KW
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX FT CDS 145..2070
XX FT /*tag= a
XX
XX W09950412-A1.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-JP01512.
XX
XX 27-MAR-1998; 98JP-0100467.
XX
XX (SAKA ) OTSUKA PHARM CO LTD.
XX PA (IKAW/) IKAWA Y.
XX
XX Ikawa Y, Ikawa S, Obinata M;
XX
XX WPI; 1999-591318/50.
XX P-PSDB; AAY45247.
XX
XX New p53 related human gene p51, useful for diagnosis, investigation and
XX treatment of cancers and screening for potential cell proliferation
XX agents -
XX
XX Example 1; Page 154-156; 163pp; Japanese.
XX
XX The present sequence represents a human p51 gene, which is related to
XX p53 and has cell proliferation regulation and tumour suppression
XX activity. The p51 gene can be used in the investigation, diagnosis and
XX treatment of diseases such as cancer, with which the p53 family cell
XX proliferation regulation is associated. The p51 protein may be used for
XX screening potential agonists and antagonists of its regulatory function,
XX for use as drugs,
XX
XX Sequence 2270 BP; 595 A; 677 C; 500 G; 498 T; 0 other;
SQ
Query Match 48.9%; Score 1376; DB 20; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGTTGATATCAAGACAGTGTGAAGGAATGAATTTTGAAGTTCACCGTGTGCCACCT 60
Db 1 TCGTTGATATCAAGACAGTGTGAAGGAATGAATTTTGAAGTTCACCGTGTGCCACCT 60
Qy 61 ACAGTACTGCTGACCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
Db 61 ACAGTACTGCTGACCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
Qy 121 AAGAAAGTTATTTACCGATCCACCATGTCAGAGACACAGACAAATGTAATTCCTCAGT 180
Db 121 AAGAAAGTTATTTACCGATCCACCATGTCAGAGACACAGACAAATGTAATTCCTCAGT 180
Qy 181 CCAGAGGTTTTCAGCATATCTGGATTTTCTGGAACAGCCTATATGTTTCAGTTCAGCCC 240
Db 181 CCAGAGGTTTTCAGCATATCTGGATTTTCTGGAACAGCCTATATGTTTCAGTTCAGCCC 240
```



Db 121 AAAGAAGTTATTACCGATCCACCATGTCCAGAGACACACAAATGAATTCCTCAGT 180  
Qy 181 CCAGAGGTTTTCAGCATATCTGGGATTTTCTGGAAACAGCCCTATATGTTTCAGTTCAGCCC 240  
Db 181 CCAGAGGTTTTCAGCATATCTGGGATTTTCTGGAAACAGCCCTATATGTTTCAGTTCAGCCC 240  
Qy 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGTTGGCAAAACAAAGATTGAGATT 300  
Db 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGTTGGCAAAACAAAGATTGAGATT 300  
Qy 301 AGCATGGAGTGTATCCGATCGAGACTCGAGACTCGAGCTGAGTGCACCCATGTGGCCACAGTAC 360  
Db 301 AGCATGGAGTGTATCCGATCGAGACTCGAGACTCGAGCTGAGTGCACCCATGTGGCCACAGTAC 360  
Qy 361 AGCAACCTGGGGCTCTCTGAACAGCATGGACAGCAGATTTCAGAACGGCTCTCTGTCACCC 420  
Db 361 AGCAACCTGGGGCTCTCTGAACAGCATGGACAGCAGATTTCAGAACGGCTCTCTGTCACCC 420  
Qy 421 AGTCCCTATAACAGACACCGCGAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAG 480  
Db 421 AGTCCCTATAACAGACACCGCGAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAG 480  
Qy 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCATCCCTCCCAACCGCATAC 540  
Db 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCATCCCTCCCAACCGCATAC 540  
Qy 541 CCAGGCCGCGACAGTTTCGAGGTGCTCTCCAGCAGTCGACACCGCCAAAGTGGCCACC 600  
Db 541 CCAGGCCGCGACAGTTTCGAGGTGCTCTCCAGCAGTCGACACCGCCAAAGTGGCCACC 600  
Qy 601 TGGACGATTCCTCACTGAACAACTCTACTGCCCAATTCGAAGACATGCCCATC 660  
Db 601 TGGACGATTCCTCACTGAACAACTCTACTGCCCAATTCGAAGACATGCCCATC 660  
Qy 661 CAGATCAAGTGTATGACCCACCTCTCAGGAGCTGTTATCGCGCCATGCTGCTAC 720  
Db 661 CAGATCAAGTGTATGACCCACCTCTCAGGAGCTGTTATCGCGCCATGCTGCTAC 720  
Qy 721 AAAAACTGAGCAGCTCAGGAGTGGTGAACGGTGGCCCAACCATGAGCTGAGCCGT 780  
Db 721 AAAAACTGAGCAGCTCAGGAGTGGTGAACGGTGGCCCAACCATGAGCTGAGCCGT 780  
Qy 781 GAATTCACAGGAGGACAGATTGCCCTCTAGTCTATTGATTCGAGTAGAGGGAACAGC 840  
Db 781 GAATTCACAGGAGGACAGATTGCCCTCTAGTCTATTGATTCGAGTAGAGGGAACAGC 840  
Qy 841 CATGCCAGTATGAGAGATCCATCAGAGGACAGAGTGTGCTGTTACCTTATGAG 900  
Db 841 CATGCCAGTATGAGAGATCCATCAGAGGACAGAGTGTGCTGTTACCTTATGAG 900  
Qy 901 CCACCCAGGTTGGCACTGAATTCAGCAGAGTCTTGTACAATTTTCATGTTGAACAGCAGT 960  
Db 901 CCACCCAGGTTGGCACTGAATTCAGCAGAGTCTTGTACAATTTTCATGTTGAACAGCAGT 960  
Qy 961 TGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAACACAGAGAT 1020  
Db 961 TGTGTTGGAGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAACACAGAGAT 1020  
Qy 1021 GGCAAGTCTCTGGCCGAGCTGCTTTGAGGCCCGGATCTGTTGCCAGGAGAGAC 1080  
Db 1021 GGCAAGTCTCTGGCCGAGCTGCTTTGAGGCCCGGATCTGTTGCCAGGAGAGAC 1080  
Qy 1081 AGGAAGCGGATGAGATAGCATAGCAAGAGCAGCAAGTTTCGACAGTAGTACAAAGACCGT 1140  
Db 1081 AGGAAGCGGATGAGATAGCATAGCAAGAGCAGCAAGTTTCGACAGTAGTACAAAGACCGT 1140  
Qy 1141 GATGTTACCAAGCGCCGTTTCGTCAGACACAGATGTTATCCAGATGACATCCATCAAG 1200  
Db 1141 GATGTTACCAAGCGCCGTTTCGTCAGACACAGATGTTATCCAGATGACATCCATCAAG 1200  
Qy 1201 AAACGAAGATCCCGAGATGATGAATGTTATCTTACCAGTGAAGGCCGCTGAGACTTAT 1260  
Db 1201 AAACGAAGATCCCGAGATGATGAATGTTATCTTACCAGTGAAGGCCGCTGAGACTTAT 1260

Qy 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTCGAATCATGTAGTACCTTCTCAGCACACA 1320  
Db 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTCGAATCATGTAGTACCTTCTCAGCACACA 1320  
Qy 1321 ATTCAAAACGTACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376  
Db 1321 ATTCAAAACGTACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376

## RESULT 7

AAF86589

ID AAF86589 standard; DNA; 2270 BP.

XX AAF86589;

AC AAF86589;

DT 03-AUG-2001 (first entry)

XX Human gene #2 used to produce a chimeric p53 gene.

XX Human; cytostatic; gene therapy; p53; human tumour; ds.

XX Homo sapiens.

XX Key

XX CDS

XX Location/Qualifiers

XX 145..2070

XX /\*tag= a

XX /product= "Human protein"

XX JF2000354488-A.

XX 26-DEC-2000.

XX 09-APR-1999; 99JP-0139034.

XX 09-APR-1999; 99JP-0139034.

XX (IKAW/) IKAWA H.

XX (SAKA ) OTSUKA PHARM CO LTD.

XX WPI: 2001-268293/28.

XX P-PSDB; AAB82129.

XX Chimera gene of the p53 family, useful for gene therapy, and treatment

XX of cancer, comprises a transcription activating region and a DNA

XX binding region -

XX Example 1; Page 40-44; 57pp; Japanese.

XX The present invention relates to a chimera gene of p53 family encoding a

XX transcription activating region, a DNA binding region, and an oligomer

XX formation region of different p53 family proteins. The chimeric gene can

XX be used for gene therapy of p53 variant human tumours, and analysis of

XX the function of the p53 family gene. The present sequence was used in the

XX present invention.

XX Query Match

XX Best Local Similarity 48.9%; Score 1376; DB 22; Length 2270;

XX Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGTATATCAAGACAGAGTTGAAGGAAATGAATTTGAAACTTTCAGGTTGCCACCT 60

Db 1 TCGTGTATATCAAGACAGAGTTGAAGGAAATGAATTTGAAACTTTCAGGTTGCCACCT 60

Qy 61 ACAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG 120

Db 61 ACAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG 120

Qy 121 AAAGAAAGTTATTATCCGATCCCATGTCCAGAGCAGACAGCAAAATGAATTCCTCAGT 180

Db 121 AAAGAAAGTTATTATCCGATCCCATGTCCAGAGCAGACAGCAAAATGAATTCCTCAGT 180

181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGSAACAGCCTATATGTTCAAGTTCAGCC 240  
181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGSAACAGCCTATATGTTCAAGTTCAGCC 240  
241 ATTGACTTGAACCTTTGGGATGAACCATCAGAGAGTGGTGGCAGCAACAGATTGAGATT 300  
241 ATTGACTTGAACCTTTGGGATGAACCATCAGAGAGTGGTGGCAGCAACAGATTGAGATT 300  
301 AGCATGGACTGTATCCGCATCGAGGACTCGGACTGAGTGCACCCCATGTGGCCACAGTAC 360  
301 AGCATGGACTGTATCCGCATCGAGGACTCGGACTGAGTGCACCCCATGTGGCCACAGTAC 360  
361 ACAGACCTGGGGTCTCTGAACAGATGACAGCAGATTCAGAACGGCTCTCTGCTCCACC 420  
361 ACAGACCTGGGGTCTCTGAACAGATGACAGCAGATTCAGAACGGCTCTCTGCTCCACC 420  
421 AGTCCCTATACACAGACCCGCGCAGACAGGCTCAGCGGCCCTCGCCCTAGCGCACAG 480  
421 AGTCCCTATACACAGACCCGCGCAGACAGGCTCAGCGGCCCTCGCCCTAGCGCACAG 480  
481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCAAACCGGACTAC 540  
481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCAAACCGGACTAC 540  
541 CCAGGCCCGCACAGTTTCGAGCTGTCTCTCCAGCAGTCGAGCAGCCGCAAGTCGGCCACC 600  
541 CCAGGCCCGCACAGTTTCGAGCTGTCTCTCCAGCAGTCGAGCAGCCGCAAGTCGGCCACC 600  
601 TGGACGTATTCGACTGAAGAACTCTACTGCCAATTTGCAAGACATGCCCCATC 660  
601 TGGACGTATTCGACTGAAGAACTCTACTGCCAATTTGCAAGACATGCCCCATC 660  
661 CAGATCAAGTGATGATGACCCACCTCTCAGGAGCTGTTATCCGCGCCATGCTGTCTAC 720  
661 CAGATCAAGTGATGATGACCCACCTCTCAGGAGCTGTTATCCGCGCCATGCTGTCTAC 720  
721 AAAAAAGCTGAGCAGCTCAGCGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780  
721 AAAAAAGCTGAGCAGCTCAGCGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780  
781 GAATTCAGCAGGACAGATGGCCCTCTAGTCAATTTGATTCAGTAGAGGGGAACAGC 840  
781 GAATTCAGCAGGACAGATGGCCCTCTAGTCAATTTGATTCAGTAGAGGGGAACAGC 840  
841 CATGCCAGTATGTAGAGATCCATCAGAGGAGCAGAGTGTGCTGACCTTATGAG 900  
841 CATGCCAGTATGTAGAGATCCATCAGAGGAGCAGAGTGTGCTGACCTTATGAG 900  
901 CCACCCAGCTGGCACTGAATTCAGCAGAGTCTTGTACAAATTCATGTCTAACAGCAGT 960  
901 CCACCCAGCTGGCACTGAATTCAGCAGAGTCTTGTACAAATTCATGTCTAACAGCAGT 960  
961 TGTGTTGAGGATGAACCCCGTCAATTTAATCAATTTGATCTCTGGAACACAGAT 1020  
961 TGTGTTGAGGATGAACCCCGTCAATTTAATCAATTTGATCTCTGGAACACAGAT 1020  
1021 GGCAAGTCTCTGGCCGACGCTCTTTGAGCGCGGATCTGCTTCCCGCAGGAAGAGC 1080  
1021 GGCAAGTCTCTGGCCGACGCTCTTTGAGCGCGGATCTGCTTCCCGCAGGAAGAGC 1080  
1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGT 1140  
1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGT 1140  
1141 GATGGTACGAAGCCCGTTTCGTGAGAACACATGGTATCCAGATGACATCCATCAAG 1200  
1141 GATGGTACGAAGCCCGTTTCGTGAGAACACATGGTATCCAGATGACATCCATCAAG 1200  
1201 AAACGAAGATCCCGATGATGAACCTTATCTTACCTAGGAGGCGCTGAGACTTAT 1260  
1201 AAACGAAGATCCCGATGATGAACCTTATCTTACCTAGGAGGCGCTGAGACTTAT 1260

1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAACCTCATGCACTACCTTCTCTCAGCACACA 1320  
1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAACCTCATGCACTACCTTCTCTCAGCACACA 1320  
1321 ATTGAACAGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376  
1321 ATTGAACAGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376  
RESULT 8  
ABL49247  
ID ABL49247 standard; cDNA; 2270 BP.  
XX  
AC ABL49247;  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE Human p53 homologue isoform, p63 (L530S) cDNA sequence S80 ID NO:332.  
XX  
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
KW immune response; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200200174-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 28-JUN-2001; 2001WO-US21065.  
XX  
PR 28-JUN-2000; 2000US-0606421.  
PR 02-AUG-2000; 2000US-0630940.  
PR 21-AUG-2000; 2000US-0643597.  
PR 15-SEP-2000; 2000US-0662786.  
PR 09-OCT-2000; 2000US-0685696.  
PR 12-DEC-2000; 2000US-0735705.  
PR 07-MAY-2001; 2001US-0850716.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
PI Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;  
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;  
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;  
XX  
WPI: 2002-090513/12.  
DR P-PSDB; ABB74990.  
XX  
PT Polynucleotides encoding lung tumor polypeptides, useful for treating  
PT lung cancer or stimulating an immune response -  
XX  
XX Example 2; Page 314-315; 374pp; English.  
XX  
CC The present invention describes human lung tumour proteins. Human lung  
CC tumour proteins and polynucleotides have cytostatic and immunostimulant  
CC activities, and can be used in vaccine production. Compositions  
CC comprising the lung tumour proteins, polynucleotides, antibodies,  
CC fusion proteins, T cell populations, or antigen presenting cells that  
CC express the lung tumour proteins are useful for treating lung cancer or  
CC stimulating an immune response. ABL4899 to ABL49300 and ABB74946 to  
CC ABB75070 represent sequences used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 2270 BP; 595.A; 676 C; 501 G; 498 T; 0 other;  
Query Match 48.9%; Score 1376; DB 24; Length 2270;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCGTGTATATCAAGACAGTGAAGGAAATGAATTTGAACCTTCAGCGTGGCCACCT 60  
Db 1 TCGTGTATATCAAGACAGTGAAGGAAATGAATTTGAACCTTCAGCGTGGCCACCT 60  
QY 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120





designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents a cDNA clone encoding human Tap63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. DeltaN isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see AX59572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Sequence 1347 BP: 374 A: 381 C: 316 G: 275 T: 1 other:

Query Match 46.0%; Score 1296; DB 20; Length 1347;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1346; Conservative 0; Mismatches 1; Indels 0;

145	ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGG	204
Qy		
1	ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGG	60
Db		
205	GATTTTCTGGACAGCCTATATGTTTCAGTTTCAGCCCATTGACTTCAACTTTGTGGATGAA	264
Qy		
61	GATTTTCTGGAAACAGCCTATATGTTTCAGTTTCAGCCCATTGACTTGAACTTTGTGGATGAA	120
Db		
265	CCATCAGAAGATGTTGGCGACAAACAAAGATTAGCATGGAGCTGTATCCGATCGAG	324
.Qy		
121	CCATCAGAAGATGTTGGCGACAAACAAAGATTAGCATGGAGCTGTATCCGATCGAG	180
Db		
325	GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACTGGGGCTCTGTAAACAGC	384
Qy		
181	GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACTGGGGCTCTGTAAACAGC	240
Db		
385	ATGGACCAGCAGATTTCAGAAGGGTCTCTGCTCCACCACTCCCTATTAACACAGACACGG	444
Qy		
241	ATGGACCAGCAGATTTCAGAAGGGTCTCTGCTCCACCACTCCCTATTAACACAGACACGG	300
Db		
445	CAGAAACAGCGTCACGGGGCCCTCGCCCTACGCCACAGCCCAAGTCCACCTTCGATGCTCTC	504
Qy		
301	CAGAAACAGCGTCACGGGGCCCTCGCCCTACGCCACAGCCCAAGTCCACCTTCGATGCTCTC	360
Db		
505	TCTCCATTACCCGGCATCCCTCTCAACACCGACTACCCAGGCCGACAGTTTTCAGACGTG	564
Qy		
361	TCCTCCATTACCCGGCCATCCCTCTCAACACCGACTACCCAGGCCGACAGTTTTCAGACGTG	420
Db		
565	TCCTTCCAGCAGTCGAGCACCGCCCAAGTCGGCCCACTCGAGCGTATTCCACTGAACTGAAG	624
Qy		
421	TCCTTCCAGCAGTCGAGCACCGCCCAAGTCGGCCCACTCGAGCGTATTCCACTGAACTGAAG	480
Db		
625	AAACTCTACTGCCCCAAATTTGAAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACT	684
Qy		
481	AAACTCTACTGCCCCAAATTTGAAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACT	540
Db		
685	CCTCAGGGAGCTGTTATCCGGGCCATGCCTGTCTACAAAAAGCTGACGACGTACGGAG	744
Qy		
541	CCTCAGGGAGCTGTTATCCGGGCCATGCCTGTCTACAAAAAGCTGACGACGTACGGAG	600
Db		
745	GTGGTGAAGCGGTGCCCCCAACCATGAGCTGAGCGTGAATTCACAGGGGACAGATTGCC	804
Qy		
601	GTGGTGAAGCGGTGCCCCCAACCATGAGCTGAGCGTGAATTCACAGGGGACAGATTGCC	660
Db		
805	CCTCCTAGTTCATTTGATTCGAGTAGAGGGGAACGCCATGCCAGTATGTAGAAGATCCC	864
Qy		
661	CCTCCTAGTTCATTTGATTCGAGTAGAGGGGAACGCCATGCCAGTATGTAGAAGATCCC	720
Db		
865	ATCACAGGAAGACAGAGTGTGCTGGTACCTTTATGAGCCACCCCGTTGGCACTGAATTC	924
Qy		

D	b	721	ATCACGGAAGACAGAGTGTCTCGTACCTTATGAGCCACCCAGGTGGCACTGAATTC	780
Q	y	925	ACGACAGTCTTGTACAAATTTTCATGTGTAAACAGCAGTGTGTGGAGGGATCAACCCGCGT	984
D	b	781	ACGACAGTCTTGTACAAATTTTCATGTGTAAACAGCAGTGTGTGGAGGGATGAACCCGCGT	840
Q	y	985	CCAATTTTAATCATTTGTACTCTCGGAACACAGAGATGGCAAGTCTCTGGCCGACGCTGC	1044
D	b	841	CCAATTTTAATCATTTGTACTCTCGGAACACAGAGATGGCAAGTCTCTGGCCGACGCTGC	900
Q	y	1045	TTTCAGGCCCGGATCTGTCTGCCAGGAAGACAGAGGCGGATGAAGATAGCATC	1104
D	b	901	TTTCAGGCCCGGATCTGTCTGCCAGGAAGACAGAGGCGGATGAAGATAGCATC	960
Q	y	1105	AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGTGTATGGTACGAAAGCCGCTTTTCGT	1164
D	b	961	AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGTGTATGGTACGAAAGCCGCTTTTCGT	1020
Q	y	1165	CAGAACACACATGGTATCCAGATGACATCCATCAAGAACGAAAGATCCCCAGATGATGAA	1224
D	b	1021	CAGAACACACATGGTATCCAGATGACATCCATCAAGAACGAAAGATCCCCAGATGATGAA	1080
Q	y	1225	CTGTATATCTTACCAGTGAAGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAGAG	1284
D	b	1081	CTGTATATCTTACCAGTGAAGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAGAG	1140
Q	y	1285	TCCCTGGAACTCATGCACTACCTTCTCAGCACACAATTTGAAACGTACAGGCAACAGCAA	1344
D	b	1141	TCCCTGGAACTCATGCACTACCTTCTCAGCACACAATTTGAAACGTACAGGCAACAGCAA	1200
Q	y	1345	CAGCAGCAGCACACGACCTTACTTTCAGAAACATCTCTTTTCAGCCTCTTCAGGAATGAG	1404
D	b	1201	CAGCAGCAGCACACGACCTTACTTTCAGAAACATCTCTTTTCAGCCTCTTCAGGAATGAG	1260
Q	y	1405	CTTGTGGAGCCCGGAGAGAACTTCCAAACAACTCTGACGCTCTTCTTAGACATTCCAAG	1464
D	b	1261	CTTGTGGAGCCCGGAGAGAACTTCCAAACAACTCTGACGCTCTTCTTAGACATTCCAAG	1320
Q	y	1465	CCCCAAACCGATCAGTGTACCCCATAG	1491
D	b	1321	CCCCAAACCGATCAGTGTACCCCATAG	1347
RESULT 10				
ID	AAZ43913	standard; cDNA; 4846 BP.		
XX	AAZ43913;			
AC	AAZ43913;			
DT	14-MAR-2000	(first entry)		
XX	Human KET	cDNA.		
DE	KET;	anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;		
KW	p53	family; angiogenic; cytotoxic; cancer; human; ss.		
XX	Homo sapiens.			
XX	WO9961610-A2.			
PN	02-DEC-1999.			
XX	25-MAY-1999;	99WO-DE01557.		
PF	25-MAY-1998;	98DE-1022985.		
XX	(FRAU )	FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.		
PI	Paul D,	Augustin M, Schmale H, Bamberger C;		
XX	WPI;	2000-062710/05.		
DR	P-PSDB;	AAY50997.		

PT  
PT

New KET-encoding nucleic acid and related proteins, for diagnosis and treatment of tumors

XX  
XX

Claim 3; Page 23-26; 28pp; German.

This invention describes a novel KET-encoding nucleic acid (I) and its fragments, variants and mutants which has anticancer activity. (I) encodes a protein, (II), involved in control of the cell cycle and apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to detect (I) in biological samples, specifically angiogenic tumor tissue, including (I) sequences that have a homozygotic deletion and (b) to detect presence or absence of human chromosome 3q27 or murine chromosome 16, or their fragments, by hybridization. Also, (I) is used as a tumor suppressor, particularly in tumors where an alteration in the wild-type p53 allele has not been identified. (I) and (II) may also be used for development of specific cytotoxic agents and for predicting the risk of developing cancer. This sequence represents the human KET cDNA sequence described in the method of the invention.

SQ Sequence 4846 BP; 1372 A; 1077 C; 990 G; 1406 T; 1 other;

Query Match 45.3%; Score 1275; DB 21; Length 4846;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	102	CCAGCTCATTTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCCAGAGACACA	161
Db	102	CCAGCTCATTTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCCAGAGACACA	161
QY	162	GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGACAGCC	221
Db	162	GACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGGGATTTCTGGACAGCC	221
QY	222	TATATGTCAGTTCAGCCCATGACTTGAATTTGTGGATGAACCATCAGAAGATGGTC	281
Db	222	TATATGTCAGTTCAGCCCATGACTTGAATTTGTGGATGAACCATCAGAAGATGGTC	281
QY	282	GACAAACAGATTGAGATTAGCATGGACTGTATCCGCATCGAGACTCGGACCTGAGTGA	341
Db	282	GACAAACAGATTGAGATTAGCATGGACTGTATCCGCATCGAGACTCGGACCTGAGTGA	341
QY	342	CCCATGTGGCCAGTACAGCAACCTGGGGCTCCTGAACAGCATGGACAGAGATTCA	401
Db	342	CCCATGTGGCCAGTACAGCAACCTGGGGCTCCTGAACAGCATGGACAGAGATTCA	401
QY	402	GAACGGCTCCTCGTCCACCATGCTTATACACAGACAGCGGCAGACAGCGTCAACGC	461
Db	402	GAACGGCTCCTCGTCCACCATGCTTATACACAGACAGCGGCAGACAGCGTCAACGC	461
QY	462	GCCTCGCCCTACGCACAGCCAGCTCCACCTCGATGCTCTCTCCATCAACCGCCAT	521
Db	462	GCCTCGCCCTACGCACAGCCAGCTCCACCTCGATGCTCTCTCCATCAACCGCCAT	521
QY	522	CCCTCCACACCGACTACCCAGCGCCGACAGTTTCGACGTGTCTTCCAGCATCGAG	581
Db	522	CCCTCCACACCGACTACCCAGCGCCGACAGTTTCGACGTGTCTTCCAGCATCGAG	581
QY	582	CACCGCCAAAGTCGGCCACCTGGACGTTATTCACCTGAAGTGAAGAACTTACTGCAAT	641
Db	582	CACCGCCAAAGTCGGCCACCTGGACGTTATTCACCTGAAGTGAAGAACTTACTGCAAT	641
QY	642	TGCAAGACATGCCCATCCAGATCAAGTGTATGATACCCCATCTCTCAGGGAGCTGTTAT	701
Db	642	TGCAAGACATGCCCATCCAGATCAAGTGTATGATACCCCATCTCTCAGGGAGCTGTTAT	701
QY	702	CCGCGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAGTGTGAAGCGGTGCC	761
Db	702	CCGCGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAGTGTGAAGCGGTGCC	761
QY	762	GAACCATGAGTGCCTGTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTCAATTGAT	821
Db	762	GAACCATGAGTGCCTGTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTCAATTGAT	821

QY	822	TCGAGTAGAGGGGAACAGCCATGCCAGTAGTATAGAAAGATCCCATCACAGAAAGACAGAG	881
Db	822	TCGAGTAGAGGGGAACAGCCATGCCAGTAGTATAGAAAGATCCCATCACAGAAAGACAGAG	881
QY	882	TGTGCTGGTACCTTATGAGCCACCCAGGTGGCACTGAATTCACGACAGCTCTTGTACAA	941
Db	882	TGTGCTGGTACCTTATGAGCCACCCAGGTGGCACTGAATTCACGACAGCTCTTGTACAA	941
QY	942	TTTCATCTGTAAACAGCAGTTGTGTGGAGGATGAACCCGCGTCCAAATTTAATCATTTGT	1001
Db	942	TTTCATCTGTAAACAGCAGTTGTGTGGAGGATGAACCCGCGTCCAAATTTAATCATTTGT	1001
QY	1002	TACTCTGAAACACAGATGGGCAAGTCTCTGGCCGACGCTGTTTGAAGCCGCGATCTG	1061
Db	1002	TACTCTGAAACACAGATGGGCAAGTCTCTGGCCGACGCTGTTTGAAGCCGCGATCTG	1061
QY	1062	TGCTTGGCCAGGAGACAGAGGCGGATGAAGATAGCATCAGAAACAGCAAGTTTC	1121
Db	1062	TGCTTGGCCAGGAGACAGAGGCGGATGAAGATAGCATCAGAAACAGCAAGTTTC	1121
QY	1122	GGACAGTACAAAGAACCGTGTATGGTACGAAGCCCGCTTTCGTCAGAACACATCGGTAT	1181
Db	1122	GGACAGTACAAAGAACCGTGTATGGTACGAAGCCCGCTTTCGTCAGAACACATCGGTAT	1181
QY	1182	CCAGATGACATCCATCAAGAAAGAGATCCCGAGATGAAGTGTATATCTTACCAGT	1241
Db	1182	CCAGATGACATCCATCAAGAAAGAGATCCCGAGATGAAGTGTATATCTTACCAGT	1241
QY	1242	GAGGGCCGTGAGACTTATGAATGCTGTGAAGATCAAGAGTCCCTGGAACATCATGCA	1301
Db	1242	GAGGGCCGTGAGACTTATGAATGCTGTGAAGATCAAGAGTCCCTGGAACATCATGCA	1301
QY	1302	GTACTTCTCAGCACACAAATTTGAACGTACAGGCAACAGCAAGCAGCAGCAGCA	1361
Db	1302	GTACTTCTCAGCACACAAATTTGAACGTACAGGCAACAGCAAGCAGCAGCAGCA	1361
QY	1362	CTTACTTCAGAAACA	1376
Db	1362	CTTACTTCAGAAACA	1376

RESULT 11

AAC66031

ID AAC66031 standard; cDNA; 4849 BP.

XX AAC66031;

XX AAC66031;

DT 21-FEB-2001 (first entry)

XX Human lung cancer-associated cDNA p63 isoform 5.

Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
vaccine; detection; ss.

XX Homo sapiens.

OS WO200061612-A2.  
XX

PN 19-OCT-2000.  
XX

PF 03-APR-2000; 2000WO-US08896.  
XX

PR 02-APR-1999; 99US-0285479.  
XX

PR 17-DEC-1999; 99US-0466396.  
XX

PR 30-DEC-1999; 99US-0476496.  
XX

PR 10-JAN-2000; 2000US-0480884.  
XX

PR 22-FEB-2000; 2000US-0510376.  
XX

PA (CORI-) CORIXA CORP.  
XX

XX Wang T, Fan L;  
XX







XX WPI; 1999-277595/23.  
DR P-PSDB; AAY05954.  
XX  
PT New isolated p63 cell regulatory protein for, e.g. treatment of  
tumours  
XX  
PS Claim 1; Fig 10; 161pp; English.  
XX  
CC The present invention concerns the discovery of a new family of  
cell regulatory proteins (CRPs) termed the p63 family of proteins,  
CC which demonstrate certain sequence identity to known tumour  
CC suppressor proteins p53 and p73. It has been observed that the  
CC intron-exon organisation is conserved between p73 and p53, and from  
CC known exon and intron sizes for these 2 genes, it was possible to  
CC identify new members of this gene family using a PCR-based strategy  
CC of amplifying 2 exons in a conserved domain and their intervening  
CC intron. The human p53 gene was localised to chromosomal position  
CC 3q27-29. At least 6 different isoforms exist. Splice variants  
CC differing at the C-terminus have been designated as alpha, beta and  
CC gamma forms, while p63 members differing in the N-terminus are  
CC designated as delta and TA forms, where the delta form lacks the  
CC transactivation domain. The present sequence represents a cDNA  
CC clone encoding human TAp63 beta. p63 was detected in a variety of  
CC human and mouse tissue. It demonstrates remarkably divergent  
CC activities, such as the ability to transactivate p53 reporter genes  
CC and induce apoptosis. Cessation or down-regulation of p63 expression  
CC may play a critical role in the process of cervical squamous  
CC differentiation, both benign and neoplastic. DeltaN isoforms of p63  
CC act as dominant negatives towards transactivation by p53 and p63.  
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
CC cachexia) and neuronal differentiation and related degenerative  
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see  
CC AAY58572-83) and anti-p63 antibodies of the invention can be used to  
CC identify compounds useful for treating disorders involving such  
CC processes, in detection and diagnosis, and in the production of  
CC transgenic animals.  
XX  
SQ Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;  
Query Match 43.8%; Score 1232; DB 20; Length 1551;  
Best Local Similarity 100.08; Pred. No. 0;  
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 145 ATGTCACAGACACACACACAAATGCTCAGTCCAGAGGTTTCCAGCATATCTGG 204  
DB 1 ATGTCACAGACACACACACAAATGCTCAGTCCAGAGGTTTCCAGCATATCTGG 60  
QY 205 GATTTCTGGAAACAGCCTATATGTTCACTGAGCCCATGACTTGAATTTGTGGAGAA 264  
DB 61 GATTTCTGGAAACAGCCTATATGTTCACTGAGCCCATGACTTGAATTTGTGGAGAA 120  
QY 265 CCATCAGAGATGTCGACAAACAGATTCAGATTAGCATGGAGTGTATCCGATGAG 324  
DB 121 CCATCAGAGATGTCGACAAACAGATTCAGATTAGCATGGAGTGTATCCGATGAG 180  
QY 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTGAAACAGC 384  
DB 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTGAAACAGC 240  
QY 385 ATGGACACAGCAGATTCAGAACGGCTCTCGTCCACAGTCCCTATAACACAGACACGCG 444  
DB 241 ATGGACACAGCAGATTCAGAACGGCTCTCGTCCACAGTCCCTATAACACAGACACGCG 300  
QY 445 CAGAACAGCTCAGCGGCGCTCGCCCTACCCACAGCCAGCTCCACCTCGATGCTCTC 504  
DB 301 CAGAACAGCTCAGCGGCGCTCGCCCTACCCACAGCCAGCTCCACCTCGATGCTCTC 360  
QY 505 TCTCCATCAGCCGCTCTCCCTCCAAACAGCAGTACCCAGCCGCGCAGTTTCGAGGTG 564  
DB 361 TCTCCATCAGCCGCTCTCCCTCCAAACAGCAGTACCCAGCCGCGCAGTTTCGAGGTG 420  
QY 565 TCCTTCCAGCAGTCGAGCAGCCGCAAGTCGCGCCACCTGGAGCTATTCACCTGAACTGAAG 624

DB 421 TCCTTCCAGCAGTCGAGCAGCCGCCAAGTCGGCCACCTGGACGTATTCACCTGAATGAAG 480  
QY 625 AAACCTACTGCCAAATTCGAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 584  
DB 481 AAACCTACTGCCAAATTCGAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 540  
QY 685 CCTCAGGAGCTGTTATCCGGGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAG 744  
DB 541 CCTCAGGAGCTGTTATCCGGGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAG 600  
QY 745 GTGGTGAAGCGGTGCCCAACCATCAGCTGAGCCGTGAATTCACAGAGGACAGATGCC 804  
DB 601 GTGGTGAAGCGGTGCCCAACCATCAGCTGAGCCGTGAATTCACAGAGGACAGATGCC 660  
QY 805 CCTCCTACTCATTTGATTTCGAGTACAGGGGACACGCTGCCCCAGTATGTAGAAGATCCC 864  
DB 661 CCTCCTACTCATTTGATTTCGAGTACAGGGGACACGCTGCCCCAGTATGTAGAAGATCCC 720  
QY 865 ATCAGAGGAACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 924  
DB 721 ATCAGAGGAACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 780  
QY 925 AGCAGAGCTTGTACAAATTTCAATGTTACAGCAGTGTGTTGGAGGATGAACCGCT 984  
DB 781 AGCAGAGCTTGTACAAATTTCAATGTTACAGCAGTGTGTTGGAGGATGAACCGCT 840  
QY 985 CCAATTTTAATCATTTTACTCTGGAACACAGAGATGGCAAGTCTTGGCCGACGCTGC 1044  
DB 841 CCAATTTTAATCATTTTACTCTGGAACACAGAGATGGCAAGTCTTGGCCGACGCTGC 900  
QY 1045 TTTGAGGCCCGGATCTGTCTTGGCCAGGAGACAGAGCGGATGAAGATGATGAA 1104  
DB 901 TTTGAGGCCCGGATCTGTCTTGGCCAGGAGACAGAGCGGATGAAGATGATGAA 960  
QY 1105 AGAAGACAGCAAGTTTCGACAGATACAAAGAACGCTGATGTGACGAAGCGCCGTTTCT 1164  
DB 961 AGAAGACAGCAAGTTTCGACAGATACAAAGAACGCTGATGTGACGAAGCGCCGTTTCT 1020  
QY 1165 CAGAACACACATGTTATCCAGATGATCCATCAAGAAACAGAGATCCCGCAGATGAA 1224  
DB 1021 CAGAACACACATGTTATCCAGATGATCCATCAAGAAACAGAGATCCCGCAGATGAA 1080  
QY 1225 CTGTTATACTTACCAAGTGGGGCGCTGAGACTTATGAAATGCTGTGAAGATCAAGAG 1284  
DB 1081 CTGTTATACTTACCAAGTGGGGCGCTGAGACTTATGAAATGCTGTGAAGATCAAGAG 1140  
QY 1285 TCCCTGGAACTCATGCTGCTCCTCAGCAGACAAATTTGAACGCTACAGGCAACAGCAA 1344  
DB 1141 TCCCTGGAACTCATGCTGCTCCTCAGCAGACAAATTTGAACGCTACAGGCAACAGCAA 1200  
QY 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1376  
DB 1201 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1232  
RESULT 14  
AAC66033  
ID AAC66033 standard; cDNA; 1551 BP.  
XX  
AC AAC66033;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE Human lung cancer-associated cDNA p63 isoform 7.  
XX  
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
XX vaccine; detection; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200061612-A2.  
XX

19-OCT-2000.  
03-APR-2000; 2000WO-US08896.  
02-APR-1999; 99US-0285479.  
17-DEC-1999; 99US-0466396.  
30-DEC-1999; 99US-0476496.  
10-JAN-2000; 2000US-0480884.  
22-FEB-2000; 2000US-0510376.  
(CORI-) CORIXA CORP.  
Wang T, Fan L;  
WPI; 2000-628399/60.  
P-PSDB; AAB11363.  
Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient.  
Claim 25a; Page 242-243; 261pp; English.  
This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from the are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2, and then administered to the patient to inhibit development of cancer.  
Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;  
Query Match 43.8%; Score 1232; DB 21; Length 1551;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
145 ATGTCCAGAGCACAGACAATGAATTCCTCAGTCCAGAGTTTCCAGCATATCTGG 204  
1 ATGTCCAGAGCACAGACAATGAATTCCTCAGTCCAGAGTTTCCAGCATATCTGG 60  
205 GATTTCTCGGAACAGCTATATGTTCAAGTTCAGTCCAGCATATCTGGATGA 264  
61 GATTTCTCGGAACAGCTATATGTTCAAGTTCAGTCCAGCATATCTGGATGA 120  
265 CCATCAGAGATGTTGCGACAACAGATTGAGATTAGCATGATGATGATGATGAT 324  
121 CCATCAGAGATGTTGCGACAACAGATTGAGATTAGCATGATGATGATGATGAT 180  
325 GACTCGGACCTGAGTGACCCATGTTGCGACAACAGATTAGCATGATGATGATGAT 384  
181 GACTCGGACCTGAGTGACCCATGTTGCGACAACAGATTAGCATGATGATGATGAT 240  
385 ATGACACAGAGATTGAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 444  
241 ATGACACAGAGATTGAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 300  
445 CAGAACAGCTGACGCGCGCTGCGCTAGCGACAGCTCCAGCTCCAGCTCCAGCT 504  
301 CAGAACAGCTGACGCGCGCTGCGCTAGCGACAGCTCCAGCTCCAGCTCCAGCT 360  
505 TCTCCATACCGCCCATCCCTCCCAACAGCTACCCAGCTCCAGCTCCAGCTCCAGCT 564  
361 TCTCCATACCGCCCATCCCTCCCAACAGCTACCCAGCTCCAGCTCCAGCTCCAGCT 420  
565 TCTCCATACCGCCCATCCCTCCCAACAGCTACCCAGCTCCAGCTCCAGCTCCAGCT 624  
421 TCTCCATACCGCCCATCCCTCCCAACAGCTACCCAGCTCCAGCTCCAGCTCCAGCT 480

QY 625 AAATCTACTGCTCAAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684  
Db 481 AAATCTACTGCTCAAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 540  
QY 685 CCTCAGGAGCTGTTATTCGCGCCATGCTGTCTACAAAAGCTGAGACAGTACGGGAG 744  
Db 541 CCTCAGGAGCTGTTATTCGCGCCATGCTGTCTACAAAAGCTGAGACAGTACGGGAG 600  
QY 745 GTGTGAAGCGGTGCCCAACCATGAGCTGAGCGGTGAATTCACAGGAGACAGATTGCC 804  
Db 601 GTGTGAAGCGGTGCCCAACCATGAGCTGAGCGGTGAATTCACAGGAGACAGATTGCC 660  
QY 805 CCTCTAGTCTATTTGATTTCGAGTAGAGGGGAAACAGCCATGCCAGTATGAGAATGCC 864  
Db 661 CCTCTAGTCTATTTGATTTCGAGTAGAGGGGAAACAGCCATGCCAGTATGAGAATGCC 720  
QY 865 ATCAGAGAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTGGGACTCAATTC 924  
Db 721 ATCAGAGAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTGGGACTCAATTC 780  
QY 925 ACGACAGTCTTGTACAAATTCATGTTGTAACAGAGTGTGTTGGAGGGATGAACCGCGT 984  
Db 781 ACGACAGTCTTGTACAAATTCATGTTGTAACAGAGTGTGTTGGAGGGATGAACCGCGT 840  
QY 985 CCAATTTTAACTGTTTACTCTGGAACCCAGAGATGGCAAGTCTCTGGCGGAGCGTGC 1044  
Db 841 CCAATTTTAACTGTTTACTCTGGAACCCAGAGATGGCAAGTCTCTGGCGGAGCGTGC 900  
QY 1045 TTTGAGGCCCGGATCTGCTGTTGCCAGAGAGACAGAGAGGCGGATGAAGATAGCATC 1104  
Db 901 TTTGAGGCCCGGATCTGCTGTTGCCAGAGAGACAGAGAGGCGGATGAAGATAGCATC 960  
QY 1105 AGAAGACAGAGTGTTCGGAGTACAAAGACCGGTGATGTGTAAGAGCCCGCTTCGT 1164  
Db 961 AGAAGACAGAGTGTTCGGAGTACAAAGACCGGTGATGTGTAAGAGCCCGCTTCGT 1020  
QY 1165 CAGAACACACATGTTATCCAGATGATCCATCAAGAAACAGAGATCCCGAGATGATGA 1224  
Db 1021 CAGAACACACATGTTATCCAGATGATCCATCAAGAAACAGAGATCCCGAGATGATGA 1080  
QY 1225 CTGTATATCTTACAGTGAAGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAG 1284  
Db 1081 CTGTATATCTTACAGTGAAGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAG 1140  
QY 1285 TCCCTGGAACCTCATGAGTACCTTCTCAGCAGACAGATTCAGAGTACAGCAACAGCAA 1344  
Db 1141 TCCCTGGAACCTCATGAGTACCTTCTCAGCAGACAGATTCAGAGTACAGCAACAGCAA 1200  
QY 1345 CAGCAGCAGCAGCAGCAGTCTACTTTCAGAAACA 1376  
Db 1201 CAGCAGCAGCAGCAGCAGTCTACTTTCAGAAACA 1232

RESULT 15  
AB149252  
ID ABL49252 standard; cDNA; 1551 bp.  
XX  
AC ABL49252;  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE Human p53 homologue isoform, p63 (L530S) cDNA sequence SEQ ID NO:337.  
XX  
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;  
XX  
KW Immune response; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200200174-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 28-JUN-2001; 2001WO-US21065.

```
XX 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX WPI: 2002-090513/12.
DR P-PSDB; ABB74995.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
XX Example 2; Page 319; 374pp; English.
XX
XX The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
CC ABB75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;
SQ
Query Match 43.8%; Score 1232; DB 24; Length 1551;
: Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 ATGCCAGAGCAGACAGACAAATGCTCTCAGTCCAGAGGTTTCCAGCATATCTGG 204
DB 1 ATGCCAGAGCAGACAGACAAATGCTCTCAGTCCAGAGGTTTCCAGCATATCTGG 60
QY 205 GATTTCCTGGAAACAGCCTATATGTTTCAGTTCAGCCCATTTGACTTGAACATTTGTGGATGAA 264
DB 61 GATTTCCTGGAAACAGCCTATATGTTTCAGTTCAGCCCATTTGACTTGAACATTTGTGGATGAA 120
QY 265 CCATCAGAAGATGTTGGGACAAACAAAGATTGAGATTAGCATGGAGTGTATCCGCATGCGAG 324
DB 121 CCATCAGAAGATGTTGGGACAAACAAAGATTGAGATTAGCATGGAGTGTATCCGCATGCGAG 180
QY 325 GACTCGGACCTGAGTGACCCCATGTCGACAGTACAGAACCTGGGGCTCCTCAACAGC 384
DB 181 GACTCGGACCTGAGTGACCCCATGTCGACAGTACAGAACCTGGGGCTCCTCAACAGC 240
QY 385 ATGGACAGCAGATTACAGAGCGGCTCCTCGCTCCACAGTCCCTATACACAGACACGCG 444
DB 241 ATGGACAGCAGATTACAGAGCGGCTCCTCGCTCCACAGTCCCTATACACAGACACGCG 300
QY 445 CAGAACAGGTCAGCGGCGGCTCGCCCTAGCCACAGCCAGCTCCACCTTCGATGCTCTC 504
DB 301 CAGAACAGGTCAGCGGCGGCTCGCCCTAGCCACAGCTCCACCTTCGATGCTCTC 360
QY 505 TCTCCATCAGCCGCTCCCTCCACACAGCTACCCAGCCGCGCCAGCTTTCGAGCTG 564
DB 361 TCTCCATCAGCCGCTCCCTCCACACAGCTACCCAGCCGCGCCAGCTTTCGAGCTG 420.
QY 565 TCCTTCAGCAGTCGAGCAGCGGCAAGTCGCGCCACCTGGAGCTATTCACCTGAACTGAAG 624
DB 421 TCCTTCAGCAGTCGAGCAGCGGCAAGTCGCGCCACCTGGAGCTATTCACCTGAACTGAAG 480
QY 625 AAATCTACTGCCAAATTTGCAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684
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Db 481 AAATCTACTGCCAAATTTGCAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 540
QY 685 CCTCAGGAGCTGTTATCCGCGCATGCTCTCTACAAAAAGCTTGACGACGTACACGGAG 744
Db 541 CCTCAGGAGCTGTTATCCGCGCATGCTCTCTACAAAAAGCTTGACGACGTACACGGAG 600
QY 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCACAGAGGGACAGATTGCC 804
Db 601 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCACAGAGGGACAGATTGCC 660
QY 805 CCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGCCATGCCAGTAGTGTAGAAGATCCC 864
Db 661 CCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGCCATGCCAGTAGTGTAGAAGATCCC 720
QY 865 ATCAGAGGAACAGAGAGTGTCTGTACTTATGAGCCACCCAGTTGGCAGCTGAATTC 924
Db 721 ATCAGAGGAACAGAGAGTGTCTGTACTTATGAGCCACCCAGTTGGCAGCTGAATTC 780
QY 925 ACAGAGTCTTTGTACAAATTTTCATGTGTAAACAGCAGTTGTGTGGAGGATGAACCGCGT 984
Db 781 ACAGAGTCTTTGTACAAATTTTCATGTGTAAACAGCAGTTGTGTGGAGGATGAACCGCGT 840
QY 985 CCAATTTTATCATTTGTTACTCTCGAAACACAGAGATGGGCAAGTCTTGGGCGGAGCTGCG 1044
Db 841 CCAATTTTATCATTTGTTACTCTCGAAACACAGAGATGGGCAAGTCTTGGGCGGAGCTGCG 900
QY 1045 TTTGAGGCGCGGATCTGTGCTTGGCCAGGAAGACAGACAGAGGCGGATGAAGATAGCATC 1104
Db 901 TTTGAGGCGCGGATCTGTGCTTGGCCAGGAAGACAGACAGAGGCGGATGAAGATAGCATC 960
QY 1105 AGAAAGCAGCAAGTTTTCGGACAGTACAAAGAACCGTGTATGTAAGAACGCGCCGTTTCGT 1164
Db 961 AGAAAGCAGCAAGTTTTCGGACAGTACAAAGAACCGTGTATGTAAGAACGCGCCGTTTCGT 1020
QY 1165 CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCAAGATGATGAA 1224
Db 1021 CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCAAGATGATGAA 1080
QY 1225 CTGTTATACTTACCAGTGAGGGCGCTGAGACTTATGAAATGCTGTTGAAGATCAAGAG 1284
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Db 1141 TCCCTGGAACTCATGCACTACCTTCTCCTCAGCACACAATTTGAACGTACAGCAACAGCAA 1200
QY 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1376
Db 1201 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1232
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Search completed: June 28, 2003, 08:12:09  
Job time : 605 secs

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Db 2341 TGTATTACCATTTTCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400
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2401 AATTTGCTTAATTTAGAGCTTCTATCCCTCAAGCCTACCTACCATTAACCAACCCATATTA 2460
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2461 CTGATAGTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTTCAGTAAAGTGAAGTCCCAAGC 2520
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Db
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Qy
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Db
2701 CACAGCACTGTATTCTTGTGACCAAGACAAATGATTTCTGTTTATTTAGGCTGTGCTT 2760
Qy
2761 TTTGTGGATGTGTGATTTTAAATTTCAATAAATTTTGCATCTTGGTTTAAAGAAA 2816
Db
2761 TTTGTGGATGTGTGATTTTAAATTTTCAATAAATTTTGCATCTTGGTTTAAAGAAA 2816
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## RESULT 4

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US-09-735-705-332
; Sequence 332, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Fongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-332
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Query Match 48.9%; Score 1376; DB 10; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAGACAGTGTGAAGGAATGAATTTTCAAACTTCACGGTGTGCCACCT 60
Db
1 TCGTTGATATCAAGACAGTGTGAAGGAATGAATTTTCAAACTTCACGGTGTGCCACCT 60
Qy
61 ACAGTACTCCCTGACCTTACATCCAGCGTTTCGTGAAGAACCCAGCTCATTTCTCTTGG 120
Db
61 ACAGTACTCCCTGACCTTACATCCAGCGTTTCGTGAAGAACCCAGCTCATTTCTCTTGG 120
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Qy 121 AAAGAAAGTTATTACCAGTCCACCATGTCCAGAGCAGACAGACAAATGAATTCCTCAGT 180
Db
121 AAAGAAAGTTATTACCAGTCCACCATGTCCAGAGCAGACAGACAAATGAATTCCTCAGT 180
Qy
181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTTCAGTTTCAGCCC 240
Db
181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTTCAGTTTCAGCCC 240
Qy
241 ATTGACTTTGAACCTTTGAGATGAACCATCAGAAAGATGGTTCGGAACAAACAGATTCGATTT 300
Db
241 ATTGACTTTGAACCTTTGAGATGAACCATCAGAAAGATGGTTCGGAACAAACAGATTCGATTT 300
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301 AGCATGGACTGTATCCGCATGTCAGGACTCGGACCTGAGTACGCCCTTACCCACAGTAC 360
Db
301 AGCATGGACTGTATCCGCATGTCAGGACTCGGACCTGAGTACGCCCTTACCCACAGTAC 360
Qy
361 ACCAACTTGGGGTCTCTGACAGCAGTGGACAGCATGGACAGCATGGACAGCATGGACAGCAT 420
Db
361 ACCAACTTGGGGTCTCTGACAGCAGTGGACAGCATGGACAGCATGGACAGCATGGACAGCAT 420
Qy
421 AGTCCCTATAACACAGACACCGCAGAACAGCGTCACGCGCCCTCGCCCTTACCCACAG 480
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421 AGTCCCTATAACACAGACACCGCAGAACAGCGTCACGCGCCCTCGCCCTTACCCACAG 480
Qy
481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAGCGCGCATCCCTTCCAAACACCCAGTAC 540
Db
481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAGCGCGCATCCCTTCCAAACACCCAGTAC 540
Qy
541 CCAGGCCCGCACAGTTTCGACGTGCTCTTCCAGCAGTGCAGCAGCCGCAAGTCGCGCCACC 600
Db
541 CCAGGCCCGCACAGTTTCGACGTGCTCTTCCAGCAGTGCAGCAGCCGCAAGTCGCGCCACC 600
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601 TGSAGCTATTCACCTGAACCTGAAGAACTCTACTGCCAAATTCGAAAGACATGCCCATC 660
Qy
661 CAGATCAAGTGTGATGACCCCTCCTCAGGAGCTGTTATCCGCGCATCCCTGTCTAC 720
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661 CAGATCAAGTGTGATGACCCCTCCTCAGGAGCTGTTATCCGCGCATCCCTGTCTAC 720
Qy
721 AAAAAAGCTGACGAGTGCAGGAGTGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
Db
721 AAAAAAGCTGACGAGTGCAGGAGTGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
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Db
781 GAATTCACAGGAGGACAGATTGCCCTCTCTAGTATGTTTCAGTAGAGGGAACAGC 840
Qy
841 CATGCCAGTATGTAGAAGTCCCATCAGGAGACAGAGTGTGCTGGTACCTTATGAG 900
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841 CATGCCAGTATGTAGAAGTCCCATCAGGAGACAGAGTGTGCTGGTACCTTATGAG 900
Qy
901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTCTGACAAATTCATGTTGTAACAGCT 960
Db
901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTCTGACAAATTCATGTTGTAACAGCT 960
Qy
961 TGTGTTGAGGAGTGAACCCCGTCCAAATTTTAACTGTTTACTCTGGAACCCAGAGAT 1020
Db
961 TGTGTTGAGGAGTGAACCCCGTCCAAATTTTAACTGTTTACTCTGGAACCCAGAGAT 1020
Qy
1021 GGGCAAGTCTCTGGCCGACGCTGTTTGGAGCCCGGATCTGTGTTGCCAGGAGAGAC 1080
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1021 GGGCAAGTCTCTGGCCGACGCTGTTTGGAGCCCGGATCTGTGTTGCCAGGAGAGAC 1080
Qy
1081 AGAAGCGGATGAAGATAGCATCAGAAAGCAGAGTTTCGACAGTACAAAGACGCT 1140
Db
1081 AGAAGCGGATGAAGATAGCATCAGAAAGCAGAGTTTCGACAGTACAAAGACGCT 1140
Qy
1141 GATGGTACCAAGCGCCGTTTCGTGAGAACACATGTTATCCAGATGACATCCATCAAG 1200
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Qy
1201 AAACGAAGATCCCCAGATGATGAACCTGTTTATATTTACCAGTGGGGCCGTGAGACTTAT 1260
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: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 332
: LENGTH: 2270
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-897-778-332

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Query Match	48.9%	Score 1376;	DB 10;	Length 2270;
Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 1376;	Conservative 0;			
QY 1	TCGTTGATATCAAGACAGTTGAAGAAATGAATTTGAAACTTCACGCTGTGCACCCCT 60			
Db				
1	TCGTTGATATCAAGACAGTTGAAGAAATGAATTTGAAACTTCACGCTGTGCACCCCT 60			
QY 61	ACAGTACTGCCCTGACCCCTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG 120			
Db				
61	ACAGTACTGCCCTGACCCCTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG 120			
QY 121	AAGAAGATTATTACCGATCCACCATGTCCAGACACACAGACAATGAATTCCTCAGT 180			
Db				
121	AAGAAGATTATTACCGATCCACCATGTCCAGACACACAGACAATGAATTCCTCAGT 180			
QY 181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGACAGCCCTATATGTTTCAGTTCAGCCC 240			
Db				
181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGACAGCCCTATATGTTTCAGTTCAGCCC 240			
QY 241	ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGGACAAACAAGATTGAGATT 300			
Db				
241	ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGGACAAACAAGATTGAGATT 300			
QY 301	AGCATGGACTGTATCCGATCGAGACTCGGACCTGAGTCACCCCATGTGGCCACAGTAC 360			
Db				
301	AGCATGGACTGTATCCGATCGAGACTCGGACCTGAGTCACCCCATGTGGCCACAGTAC 360			
QY 361	AGAACTGGGGCTCTCTGAACAGATGGACAGAGATTCAGAACCGCTCTCTGTCACCC 420			
Db				
361	AGAACTGGGGCTCTCTGAACAGATGGACAGAGATTCAGAACCGCTCTCTGTCACCC 420			
QY 421	AGTCCCTATAACACAGACACGGCGACAGCGTACGCGCCCTCGCCCTACGCACAG 480			
Db				
421	AGTCCCTATAACACAGACACGGCGACAGCGTACGCGCCCTCGCCCTACGCACAG 480			
QY 481	CCAGCTCCACCTTCGATGCTCTCTCTCCATCACCGCCATCCCTCCACACACGACTAC 540			
Db				
481	CCAGCTCCACCTTCGATGCTCTCTCTCCATCACCGCCATCCCTCCACACACGACTAC 540			
QY 541	CCAGGCCCGCACAGTTTCGAGTGTCTTCCAGCAGTCGAGCAGCCGCAAGTCGGCCACC 600			
Db				
541	CCAGGCCCGCACAGTTTCGAGTGTCTTCCAGCAGTCGAGCAGCCGCAAGTCGGCCACC 600			
QY 601	TGGACGPTATCCACTGAACTGAAGAACTCTACTGCCAAATTCGAAGACATGCCCATC 660			
Db				
601	TGGACGPTATCCACTGAACTGAAGAACTCTACTGCCAAATTCGAAGACATGCCCATC 660			
QY 661	CAGATCAAGGTGATGACCCCACTCCTCAGGAGCTGTTATCCCGGCATTCGCTGCTAC 720			
Db				
661	CAGATCAAGGTGATGACCCCACTCCTCAGGAGCTGTTATCCCGGCATTCGCTGCTAC 720			
QY 721	AAAAAGCTGAGCAGTTCACGAGGTGTTGAAGCGGTGCCCCCAACATGAGCTGAGCCGT 780			
Db				
721	AAAAAGCTGAGCAGTTCACGAGGTGTTGAAGCGGTGCCCCCAACATGAGCTGAGCCGT 780			
QY 781	GAAATTCACGAGGACAGATTGCCCTCTTAGTTCATTTGATTCGAGTAGAGGGACACG 840			
Db				
781	GAAATTCACGAGGACAGATTGCCCTCTTAGTTCATTTGATTCGAGTAGAGGGACACG 840			
QY 841	CATGCCCACTATGTAGAAGATCCCATCACAGGACAGAGTGTGCTGCTATGAG 900			

## RESULT 7

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US-09-735-705-335
; Sequence 335, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735.705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-335

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	Query Match	45.3%	Score 1275;	DB 10;	Length 4849;
	Best Local Similarity	100.08;	Pred. No. 0;		
	Matches 1275;	Conservative	0;	Mismatches	0;
				Indels	Gaps
QY	102	CCGAGCTCATTTCTCTTGGAAAGAAAGCTTTATTACGATCCACCATCTCCAGAGCACACA	161		
Db	102	CCGAGCTCATTTCTCTTGGAAAGAAAGCTTTATTACGATCCACCATCTCCAGAGCACACA	161		



162 GACAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGGGATTTCTTGGAAACAGCC 221  
162 GACAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGGGATTTCTTGGAAACAGCC 221  
222 TATATGTTCACTTCAGCCCATGTACTGAACTTTGTGGATGAACCATCAGAAAGATGGTC 281  
222 TATATGTTCACTTCAGCCCATGTACTGAACTTTGTGGATGAACCATCAGAAAGATGGTC 281  
282 GACAAACAAAGATTAGCATGGAGTGTATCCGATCGAGACTCGGACCTGAGTGA 341  
282 GACAAACAAAGATTAGCATGGAGTGTATCCGATCGAGACTCGGACCTGAGTGA 341  
342 CCCCATGTGGCCACAGTACAGAACTCGGGCTCCTGAACAGCATGGACACAGAGATTCA 401  
342 CCCCATGTGGCCACAGTACAGAACTCGGGCTCCTGAACAGCATGGACACAGAGATTCA 401  
402 GAACGGCTCTCTGTCACAGTCCCTATAACACAGACACCGCGGAGAACAGCGTCACGGC 461  
402 GAACGGCTCTCTGTCACAGTCCCTATAACACAGACACCGCGGAGAACAGCGTCACGGC 461  
462 GCGCTCGCCCTACGACAGCCAGCTCCACCTTCGATGCTCTCTCTCATCACCAGCAT 521  
462 GCGCTCGCCCTACGACAGCCAGCTCCACCTTCGATGCTCTCTCTCATCACCAGCAT 521  
522 CCCCTCCAACACCGACTACCCAGCCCGCAGTTCGACGTGCTCTTCCAGCAGTCGAG 581  
522 CCCCTCCAACACCGACTACCCAGCCCGCAGTTCGACGTGCTCTTCCAGCAGTCGAG 581  
582 CACCGCCAAAGTCGCGCCACCTGGAGTATTCACCTGAACCTGAAGAACTCTACTGCCAAAT 641  
582 CACCGCCAAAGTCGCGCCACCTGGAGTATTCACCTGAACCTGAAGAACTCTACTGCCAAAT 641  
642 TGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCTCCTCAGGAGCTGTAT 701  
642 TGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCTCCTCAGGAGCTGTAT 701  
702 CCGCGCCATGCTCTGTACAAAAGCTGAGCAGCTCAGGAGTGTGTAAGCGGTGCC 761  
702 CCGCGCCATGCTCTGTACAAAAGCTGAGCAGCTCAGGAGTGTGTAAGCGGTGCC 761  
762 CAACCATGAGCTGAGCGTGAATTCACGAGGGACAGATTGCCCTCCTAGTCATTGTAT 821  
762 CAACCATGAGCTGAGCGTGAATTCACGAGGGACAGATTGCCCTCCTAGTCATTGTAT 821  
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882 TGTGCTGCTACCTTATGAGCCACCCAGTGGCACTGAATTCAGCAGTCTTTGTACAA 941  
882 TGTGCTGCTACCTTATGAGCCACCCAGTGGCACTGAATTCAGCAGTCTTTGTACAA 941  
942 TTTTCATGTTAAGCAGCTGTGTGGAGGATGAACCGCGCTCCAATTTAATCATGT 1001  
942 TTTTCATGTTAAGCAGCTGTGTGGAGGATGAACCGCGCTCCAATTTAATCATGT 1001  
1002 TACTCTGGAACACAGAGATGGCAAGTCTTGGCGGAGCTGCTTGGAGCCCGGATCTG 1061  
1002 TACTCTGGAACACAGAGATGGCAAGTCTTGGCGGAGCTGCTTGGAGCCCGGATCTG 1061  
1062 TGCTTGCCAGGAAGAGACAGAAAGGCGGATGAAGATAGCATCAAGAAAGCAGATGTC 1121  
1062 TGCTTGCCAGGAAGAGACAGAAAGGCGGATGAAGATAGCATCAAGAAAGCAGATGTC 1121  
1122 GGACAGTACAAGAACGGTGTATGTACGAAGCGCCGCTTTCGTTCAGAACACATGGTAT 1181  
1122 GGACAGTACAAGAACGGTGTATGTACGAAGCGCCGCTTTCGTTCAGAACACATGGTAT 1181  
1182 CCAGATGACATCCATCAAGAAACGAGATCCCAAGATGATGAATGTTTATCTTACCAGT 1241  
1182 CCAGATGACATCCATCAAGAAACGAGATCCCAAGATGATGAATGTTTATCTTACCAGT 1241  
1242 GAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCA 1301

1242 GAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCA 1301  
1302 GTACTTCTCAGCAGACACAATTTGAACGTACAGGCAACAGCAGCAGCAGCAGCA 1361  
1302 GTACTTCTCAGCAGACACAATTTGAACGTACAGGCAACAGCAGCAGCAGCAGCA 1361  
1362 CTTACTTTCAGAAACA 1376  
1362 CTTACTTCAGAAACA 1376  
RESULT 8  
US-09-850-716A-335  
; Sequence 335, Application US/09850716A  
; Patent No. US20020115139A1  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 335  
; LENGTH: 4849  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-850-716A-335  
Query Match 45.3%; Score 1275; DB 10; Length 4849;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 102 CCCAGCTCATTTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCCAGAGCAGCACA 161  
DB 102 CCCAGCTCATTTCTTGGAAAGAAAGTTATTACCGATCCACCATGTCCAGAGCAGCACA 161  
QY 162 GACAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGGGATTTCTTGGAAACAGCC 221  
DB 162 GACAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGGGATTTCTTGGAAACAGCC 221  
QY 222 TATATGTTCACTTCAGCCCATGTACTGAACTTTGTGGATGAACCATCAGAAAGATGGTGC 281  
DB 222 TATATGTTCACTTCAGCCCATGTACTGAACTTTGTGGATGAACCATCAGAAAGATGGTGC 281  
QY 282 GACAAACAAAGATTAGATTAGCATGGAGTGTATCCGCATCGAGGACTCGGACCTGAGTGA 341  
DB 282 GACAAACAAAGATTAGATTAGCATGGAGTGTATCCGCATCGAGGACTCGGACCTGAGTGA 341  
QY 342 CCCCATGTGGCCACAGTACAGAACTCGGGCTCCTGAACAGCATGGACACAGCAGATTCA 401  
DB 342 CCCCATGTGGCCACAGTACAGAACTCGGGCTCCTGAACAGCATGGACACAGCAGATTCA 401  
QY 402 GAACGGCTCTCTGTCACAGTCCCTATAACACAGACACCGCGGAGAACAGCGTCACGGC 461  
DB 402 GAACGGCTCTCTGTCACAGTCCCTATAACACAGACACCGCGGAGAACAGCGTCACGGC 461  
QY 462 GCGCTCGCCCTACGACAGCCAGCTCCACCTTCGATGCTCTCTCTCATCACCAGCAT 521  
DB 462 GCGCTCGCCCTACGACAGCCAGCTCCACCTTCGATGCTCTCTCTCATCACCAGCAT 521  
QY 522 CCCCTCCAACACCGACTACCCAGCCCGCAGTTCGACGTGCTCTTCCAGCAGTCGAG 581  
DB 522 CCCCTCCAACACCGACTACCCAGCCCGCAGTTCGACGTGCTCTTCCAGCAGTCGAG 581  
QY 582 CACCGCCAAAGTCGCGCCACCTGGAGTATTCACCTGAACCTGAAGAACTCTACTGCCAAAT 641  
DB 582 CACCGCCAAAGTCGCGCCACCTGGAGTATTCACCTGAAGAACTCTACTGCCAAAT 641







## RESULT 11

US-09-850-716A-337  
; Sequence 337, Application US/09850716A  
; Patent No. US20020115139A1  
; GENERAL INFORMATION:

; APPLICANT: Kelos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A

; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 337

; LENGTH: 1551

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-850-716A-337

Query Match 43.8%; Score 1232; DB 10; Length 1551;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	145	ATGTCCAGAGCAGACAGACAAATGAAATCTCCAGTCCAGAGGTTTCCAGCATATCTGG	204
Db	1	ATGTCCAGAGCAGACAGACAAATGAAATCTCCAGTCCAGAGGTTTCCAGCATATCTGG	60
QY	205	GATTTCTGGAACAGCCTATATGTTGATTCAGTTCAGCCCATTTGAACTTTTGGATGAA	264
Db	61	GATTTCTGGAACAGCCTATATGTTGATTCAGTTCAGCCCATTTGAACTTTTGGATGAA	120
QY	265	CCATCAGAGATGGTGGCAGAAACAGATTCAGATTCAGATTCAGATTCAGATTCAGAT	324
Db	121	CCATCAGAGATGGTGGCAGAAACAGATTCAGATTCAGATTCAGATTCAGATTCAGAT	324
QY	325	GACTCGGACCTGAGTGACCCCATGTTGAGTTCAGTTCAGCCCATTTGAACTTTTGGATGAA	384
Db	181	GACTCGGACCTGAGTGACCCCATGTTGAGTTCAGTTCAGCCCATTTGAACTTTTGGATGAA	384
QY	385	ATGGACAGCAGATTCAGAACGGCTCTGCTGACACAGTCCCTATACAGACAGACCGG	444
Db	241	ATGGACAGCAGATTCAGAACGGCTCTGCTGACACAGTCCCTATACAGACAGACCGG	444
QY	445	CAGAACAGCAGTCCAGGCGGCTGCTGCTGACACAGTCCCTATACAGACAGACCGG	504
Db	301	CAGAACAGCAGTCCAGGCGGCTGCTGCTGACACAGTCCCTATACAGACAGACCGG	504
QY	505	TCTCCATCAGCCGCTCCCTCCACACAGTCCCTATACAGACAGTCCCTATACAGACAG	564
Db	361	TCTCCATCAGCCGCTCCCTCCACACAGTCCCTATACAGACAGTCCCTATACAGACAG	564
QY	565	TCCTTCCAGAGTCCAGGCGGCTGCTGCTGACACAGTCCCTATACAGACAGTCCCTAT	624
Db	421	TCCTTCCAGAGTCCAGGCGGCTGCTGCTGACACAGTCCCTATACAGACAGTCCCTAT	624
QY	625	AAACTCTAGTCCAAATTCAGAACAGATCCCTATACAGACAGTCCCTATACAGACAG	684
Db	481	AAACTCTAGTCCAAATTCAGAACAGATCCCTATACAGACAGTCCCTATACAGACAG	684
QY	685	CCTCAGGAGCTTATCCGCGGCTGCTGCTGACACAGTCCCTATACAGACAGTCCCTAT	744
Db	541	CCTCAGGAGCTTATCCGCGGCTGCTGCTGACACAGTCCCTATACAGACAGTCCCTAT	744
QY	745	GTGGTGAAGCGTCCGCGGCTGCTGCTGACACAGTCCCTATACAGACAGTCCCTATAC	804
Db	601	GTGGTGAAGCGTCCGCGGCTGCTGCTGACACAGTCCCTATACAGACAGTCCCTATAC	804
QY	805	CCTCTAGTTCATTTGATTCAGAGTCCGCGGCTGCTGCTGACACAGTCCCTATACAG	864
Db	661	CCTCTAGTTCATTTGATTCAGAGTCCGCGGCTGCTGCTGACACAGTCCCTATACAG	864

QY	865	ATCAGAGAGACAGAGTGTGCTGATCTTATCAGCCACCCAGGTTGCACTGATTC	924
Db	721	ATCAGAGAGACAGAGTGTGCTGATCTTATCAGCCACCCAGGTTGCACTGATTC	924
QY	925	ACGACAGTCTTGTACAAATTTTCATGTTAACAGCAGTGTGTTGGAGGGATGAACCCCGT	984
Db	781	ACGACAGTCTTGTACAAATTTTCATGTTAACAGCAGTGTGTTGGAGGGATGAACCCCGT	984
QY	985	CCAATTTTAATCATTTGTTACTCTGGAAACCCAGAGATGGCAAGTCTGCGGCGAGCTGC	1044
Db	841	CCAATTTTAATCATTTGTTACTCTGGAAACCCAGAGATGGCAAGTCTGCGGCGAGCTGC	1044
QY	1045	TTTGAGGCCCGGATCTGTGCTTCCAGGAGAGACAGGAGCGGATGAAGATAGCATC	1104
Db	901	TTTGAGGCCCGGATCTGTGCTTCCAGGAGAGACAGGAGCGGATGAAGATAGCATC	1104
QY	1105	AGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGTGTGTTGACGAAGCGGCTTTCGT	1164
Db	961	AGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGTGTGTTGACGAAGCGGCTTTCGT	1164
QY	1165	CAGAACACATGTTATCCAGATGATCCATCAAGAACGAAGATCCCAAGATGATGAA	1224
Db	1021	CAGAACACATGTTATCCAGATGATCCATCAAGAACGAAGATCCCAAGATGATGAA	1224
QY	1225	CTGTTATCTTACAGTGTAGGCGGCTGAGACTTATGAAATCTGTTGAAGATCAAGAG	1284
Db	1081	CTGTTATCTTACAGTGTAGGCGGCTGAGACTTATGAAATCTGTTGAAGATCAAGAG	1284
QY	1285	TCCTTGGAACTCATCAGTCTTCTCAGCAGCAATTTGAAATCTGTTGAAGATCAAGAG	1344
Db	1141	TCCTTGGAACTCATCAGTCTTCTCAGCAGCAATTTGAAATCTGTTGAAGATCAAGAG	1344
QY	1345	CAGCAGAGCAGCAGCAGTCTTCTCAGCAGCAATTTGAAATCTGTTGAAGATCAAGAG	1404
Db	1201	CAGCAGAGCAGCAGCAGTCTTCTCAGCAGCAATTTGAAATCTGTTGAAGATCAAGAG	1404

## RESULT 12

US-09-897-778-337

; Sequence 337, Application US/09897778

; Patent No. US20020147143A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tonglong

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Peckham, David W.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 337

; LENGTH: 1551

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-897-778-337

Query Match 43.8%; Score 1232; DB 10; Length 1551;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	145	ATGTCCAGAGCAGACAGACAAATGAAATCTCCAGTCCAGAGGTTTCCAGCATATCTGG	204
Db	1	ATGTCCAGAGCAGACAGACAAATGAAATCTCCAGTCCAGAGGTTTCCAGCATATCTGG	60
QY	205	GATTTCTGGAACAGCCTATATGTTGATTCAGTTCAGCCCATTTGAACTTTTGGATGAA	264

Db 61 GATTTCTGGAAAGCCTATATGTTCAAGTTCAGCCCATTTGACTTTGATGAA 120  
QY 265 CCATCAGAGATGTCGGACAAACAAGATTAGATTAGCATGGACTGATCCGATCGAG 324  
Db 121 CCATCAGAGATGTCGGACAAACAAGATTAGATTAGCATGGACTGATCCGATCGAG 180  
QY 325 GACTCGGACCTGAGTCAGCCCATGTCGGCCACAGTACAGAACTGGGGCTCCTGAACAGC 384  
Db 181 GACTCGGACCTGAGTCAGCCCATGTCGGCCACAGTACAGAACTGGGGCTCCTGAACAGC 240  
QY 385 ATGACACAGCATTCAGAACGGCTCTCTGTCACACAGTCCCTATAACACAGACACGCG 444  
Db 241 ATGACACAGCATTCAGAACGGCTCTCTGTCACACAGTCCCTATAACACAGACACGCG 300  
QY 445 CAGAACAGCTCAGCGGCGCTCGCCCTACGACAGCCAGCTCCACTTCGATGCTCTC 504  
Db 301 CAGAACAGCTCAGCGGCGCTCGCCCTACGACAGCCAGCTCCACTTCGATGCTCTC 360  
QY 505 TCTCCATCACCGCCATCCCTCCAAACACCGACTACCCAGCGCCGACAGTTTCGACGTG 564  
Db 361 TCTCCATCACCGCCATCCCTCCAAACACCGACTACCCAGCGCCGACAGTTTCGACGTG 420  
QY 565 TCCTTCCAGCAGTCGAGACCGCCAAAGTCGCGCCACCTGGAGGTATTCACCTGAAG 624  
Db 421 TCCTTCCAGCAGTCGAGACCGCCAAAGTCGCGCCACCTGGAGGTATTCACCTGAAG 480  
QY 625 AAATCTACTGCCAAATTCGAAACATGCCCCATCCAGATCAAGGTGATGACCCACCT 684  
Db 481 AAATCTACTGCCAAATTCGAAACATGCCCCATCCAGATCAAGGTGATGACCCACCT 540  
QY 685 CCTCAGGAGCTGTTATCCGGCGCATGCTCTACAAAAAGCTGACAGCTCACGGAG 744  
Db 541 CCTCAGGAGCTGTTATCCGGCGCATGCTCTCTACAAAAAGCTGACAGCTCACGGAG 600  
QY 745 GTGTGAAGCGGTGCCCAACCATGAGTGAAGCTGAAATTCACAGGGACAGATTGCC 804  
Db 601 GTGTGAAGCGGTGCCCAACCATGAGTGAAGCTGAAATTCACAGGGACAGATTGCC 660  
QY 805 CCTCCTAGCTATTTGATTCAGTAGAGGGACAGCCATGCCAGTATGTAGAGATCCC 864  
Db 661 CCTCCTAGCTATTTGATTCAGTAGAGGGACAGCCATGCCAGTATGTAGAGATCCC 720  
QY 865 ATCAGAGAACAGAGAGTGTCTGCTTATGAGCCACCCAGGTGGCACTGAATTC 924  
Db 721 ATCAGAGAACAGAGAGTGTCTGCTTATGAGCCACCCAGGTGGCACTGAATTC 780  
QY 925 ACGACAGTCTGTGTAACATTTGATGTAACAGCAGTTGTGTTGAGGAGTGAACCGCGT 984  
Db 781 ACGACAGTCTGTGTAACATTTGATGTAACAGCAGTTGTGTTGAGGAGTGAACCGCGT 840  
QY 985 CCAATTTTAATCATTTGTTACTCTGGAACACAGAGATGGCAAGTCTCTGGCGCGAGTGC 1044  
Db 841 CCAATTTTAATCATTTGTTACTCTGGAACACAGAGATGGCAAGTCTCTGGCGCGAGTGC 900  
QY 1045 TTTGAGGCCCGGATCTGTCTGTCAGGAAGACAGAGAGGGCGGATGAAGATAGCATC 1104  
Db 901 TTTGAGGCCCGGATCTGTCTGTCAGGAAGACAGAGAGGGCGGATGAAGATAGCATC 960  
QY 1105 AGAAGCAGCAAGTTTCGGACAGTACAAAGACCGGTGATGTTAGACGCGCCGTTTCGT 1164  
Db 961 AGAAGCAGCAAGTTTCGGACAGTACAAAGACCGGTGATGTTAGACGCGCCGTTTCGT 1020  
QY 1165 CAGAACACATGCTATCCAGATGACATCCATCAAGAACCAAGATCCCCAGATGATGAA 1224  
Db 1021 CAGAACACATGCTATCCAGATGACATCCATCAAGAACCAAGATCCCCAGATGATGAA 1080  
QY 1225 CTGTTATACTTACCAAGTGAGGGCGGTGAGACTTATGAAATGCTGTTGAAGTCAAGAG 1284  
Db 1081 CTGTTATACTTACCAAGTGAGGGCGGTGAGACTTATGAAATGCTGTTGAAGTCAAGAG 1140  
QY 1285 TCCCTGGAACCTATGCAAGTACCTTCTCAGCACACAATTTGAACAGTACAGCAACAGCAA 1344

Db 1141 TCCCTGGAACTCATGTCAGTACTTCTCAGCACACAATTTGAACGTACAGCAACAGCAA 1200  
QY 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1376  
Db 1201 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACA 1232  
RESULT 13  
US-09-735-705-336  
; Sequence 336, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 336  
; LENGTH: 1386  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-735-705-336  
Query Match 36.4%; Score 1026; DB 10; Length 1386;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1026; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 351 GCCACAGTACACGAACTTGGGGCTCTCGAACAGCATGACGACGAGATTCAGAACGGCTC 410  
Db 42 GCCACAGTACACGAACTTGGGGCTCTCGAACAGCATGACGACGAGATTCAGAACGGCTC 101  
QY 411 CTGCTCAGCAGTCCCTATACACAGACCGCGCAGAACAGCGTCAAGCGGCGCTCGCC 470  
Db 102 CTGCTCAGCAGTCCCTATACACAGACCGCGCAGAACAGCGTCAAGCGGCGCTCGCC 161  
QY 471 CTAGCGACAGCCCGACGCTCCAGTCTCTCTCTCCATCACCGCGCATCCCTCCAA 530  
Db 162 CTAGCGACAGCCCGACGCTCCAGTCTCTCTCTCCATCACCGCGCATCCCTCCAA 221  
QY 531 CACGACATACCCAGCGCGCACAGTTTCGAGCTGTCTTCCAGCAGTTCGAGACCGCCAA 590  
Db 222 CACGACATACCCAGCGCGCACAGTTTCGAGCTGTCTTCCAGCAGTTCGAGACCGCCAA 281  
QY 591 GTCGGCCACTTGGAGCTATTCCTGAACTGAAGAACTCTACTGCCAAATTCGAAAGAC 650  
Db 282 GTCGGCCACTTGGAGCTATTCCTGAACTGAAGAACTCTACTGCCAAATTCGAAAGAC 341  
QY 651 ATGCCCATCCAGATCAAGGTGATGACCCACCTCTCTCAGGAGCTGTATCCGGCGCAT 710  
Db 342 ATGCCCATCCAGATCAAGGTGATGACCCACCTCTCTCAGGAGCTGTATCCGGCGCAT 401  
QY 711 GCCTGTCTACAAAAAGCTGACAGCTCAGCGAGTGGTGAAGCGGTGCCCAACCATGA 770  
Db 402 GCCTGTCTACAAAAAGCTGACAGCTCAGCGAGTGGTGAAGCGGTGCCCAACCATGA 461  
QY 771 GCTGAGCGCTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTATTTGATTTCGAGTGA 830  
Db 462 GCTGAGCGCTGAATTCACAGGAGGACAGATTGCCCTCTCTAGTATTTGATTTCGAGTGA 521



; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Derrick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 336  
; LENGTH: 1386  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
us-09-897-778-336

Query Match 36.4%; Score 1026; DB 10; Length 1386;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1026; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	351	GCACAGTACACGAACCTGGGGCTCTCTGAACAGCATGGACCAGCAGATTTCAGAACGGCTC	410
Db	42	GCACAGTACACGAACCTGGGGCTCTCTGAACAGCATGGACCAGCAGATTTCAGAACGGCTC	101
Qy	411	CTGCTCCACCACTCCCTATACACAGACACGCGGCGAGACAGCGTTCAGCGGCGCTCGCC	470
Db	102	CTGCTCCACCACTCCCTATACACAGACACGCGGCGAGACAGCGTTCAGCGGCGCTCGCC	161
Qy	471	CTAGGCACAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCCATCCCTCCAA	530
Db	162	CTAGGCACAGCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCCATCCCTCCAA	221
Qy	531	CACCGACTACCCAGGCGCCGACAGTTTCAGCTGTCTCCAGCAGTCGAGCACCAGCAA	590
Db	222	CACCGACTACCCAGGCGCCGACAGTTTCGAGCTGTCTCCAGCAGTCGAGCACCAGCAA	281
Qy	591	GTGCGCCACCTGACGCTATTCACCTGACTGACTGACTGACTGACTGACTGACTGACTG	650
Db	282	GTGCGCCACCTGACGCTATTCACCTGACTGACTGACTGACTGACTGACTGACTGACTG	341
Qy	651	ATGCCCATCCAGATCAAGTGATGACCCACCTCTCTCAGGAGCTGTATTCGCGCAT	710
Db	342	ATGCCCATCCAGATCAAGTGATGACCCACCTCTCTCAGGAGCTGTATTCGCGCAT	401
Qy	711	GCCTGTCTACAAAAAGCTGAGCAGCTCACGGAGTGGTGAAGCGTGCCCCCAACCATGA	770
Db	402	GCCTGTCTACAAAAAGCTGAGCAGCTCACGGAGTGGTGAAGCGTGCCCCCAACCATGA	461
Qy	771	GCTGAGCCGTGAATTCACAGGAGCAGATTGCCCCCTCTAGTCATTGATTCGAGTAGA	830
Db	462	GCTGAGCCGTGAATTCACAGGAGCAGATTGCCCCCTCTAGTCATTGATTCGAGTAGA	521
Qy	831	GGGGAACAGCCATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGTGT	890
Db	522	GGGGAACAGCCATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGTGT	581
Qy	891	ACCTTATGAGCCACCCAGGTGGCAGTGAATTCAGACAGTCTTGTACAAATTTCAATGTG	950
Db	582	ACCTTATGAGCCACCCAGGTGGCAGTGAATTCAGACAGTCTTGTACAAATTTCAATGTG	641
Qy	951	TACAGCAGTGTGTGGAGGATGAACCCCGTCCAAATTTAATCAATTTACTCTGGA	1010
Db	642	TACAGCAGTGTGTGGAGGATGAACCCCGTCCAAATTTAATCAATTTACTCTGGA	701
Qy	1011	AACCAGAGTGGGCAAGTCTCTGGCGCAGCTCTTGTAGGCGCGGATCTGTCTGCC	1070
Db	702	AACCAGAGTGGGCAAGTCTCTGGCGCAGCTCTTGTAGGCGCGGATCTGTCTGCC	761
Qy	1071	AGGAAGAGACAGGAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTAC	1130

Search completed: June 28, 2003, 11:17:30

Job time : 404 secs

Db	762	AGGAAGAGACAGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTAC	821
Qy	1131	AAAGAACGGTGATGGTAGAAGCCCGTTTCGTCAAGAACACACATGGTATCCAGATGAC	1190
Db	822	AAAGAACGGTGATGGTAGAAGCCCGTTTCGTCAAGAACACACATGGTATCCAGATGAC	881
Qy	1191	ATCCATCAAGAAAGAAAGATCCCCAGATGATGAACCTGTATATCTTACCAGTGAGGGCG	1250
Db	882	ATCCATCAAGAAAGAAAGATCCCCAGATGATGAACCTGTATATCTTACCAGTGAGGGCG	941
Qy	1251	TGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTCGAAGTCTCATGAGTACCTTCC	1310
Db	942	TGAGACTTATGAATGCTGTTGAAGATCAAGAGTCCCTCGAAGTCTCATGAGTACCTTCC	1001
Qy	1311	TCAGCACACAATTGAACAGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAG	1370
Db	1002	TCAGCACACAATTGAACAGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAG	1061
Qy	1371	GAACA 1376	
Db	1062	GAACA 1067	

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:12:06 ; Search time 36 Seconds  
(without alignments)  
2564.142 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 448

Sequence: 1 MSQSTQTFNEFLSPVFOH.....PKQSDVFFRHSKPPNRSVYP 448

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_21.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	487	4 Q9H3D2	Q9h3d2 homo sapien
2	410	91.5	471	4 Q9NPH7	Q9nph7 homo sapien
3	410	91.5	516	4 Q9P1B7	Q9plb7 homo sapien
4	410	91.5	555	4 Q9H3D3	Q9h3d3 homo sapien
5	410	91.5	641	4 Q75195	Q75195 homo sapien
6	410	91.5	680	4 Q9UE10	Q9ue10 homo sapien
7	410	91.5	680	4 Q9H3B4	Q9h3b4 homo sapien
8	379	84.6	393	4 Q75922	Q75922 homo sapien
9	341	76.1	416	4 Q9P1B6	Q9plb6 homo sapien
10	341	76.1	461	4 Q9P1B5	Q9plb5 homo sapien
11	341	76.1	461	4 Q9UP26	Q9up26 homo sapien
12	341	76.1	586	4 Q9P1B4	Q9plb4 homo sapien
13	341	76.1	586	4 Q9UBV9	Q9ubv9 homo sapien
14	284	63.4	483	11 O88897	O88897 mus musculus
15	284	63.4	555	11 Q9QWZ0	Q9qwz0 mus musculus
16	284	63.4	680	11 O88898	O88898 mus musculus

17	272	60.7	586	4	O75080	O75080 homo sapien
18	269	60.0	356	4	O9UP74	O9up74 homo sapien
19	259	57.8	389	11	O88899	O88899 mus musculus
20	259	57.8	461	11	O9QWY9	O9qw9 mus musculus
21	259	57.8	586	11	O89097	O89097 mus musculus
22	256	57.1	501	4	O9H3P8	O9h3p8 homo sapien
23	248	55.4	393	11	O99JD9	O99jd9 rattus norv
24	248	55.4	461	11	O99JD6	O99jd6 rattus norv
25	248	55.4	470	11	O99JE1	O99jel rattus norv
26	248	55.4	487	11	O99JE0	O99je0 rattus norv
27	248	55.4	538	11	O99JD7	O99jd7 rattus norv
28	248	55.4	555	11	O99JD8	O99jd8 rattus norv
29	248	55.4	586	11	O99JE2	O99je2 rattus norv
30	248	55.4	663	11	O99JE3	O99je3 rattus norv
31	248	55.4	680	11	O9JJP6	O9jip6 rattus norv
32	220	49.1	232	4	O96KR0	O96kr0 homo sapien
33	137	30.6	582	13	O9DEC7	O9dec7 gallus gall
34	95	21.2	365	13	O98SW0	O98sw0 xenopus lae
35	22	4.9	450	4	O8TDY5	O8tdy5 homo sapien
36	22	4.9	587	4	O8TDY6	O8tdy6 homo sapien
37	22	4.9	641	13	O9W664	O9w664 barbus barb
38	20	4.5	514	11	O9CU77	O9cu77 mus musculus
39	20	4.5	590	11	O9JJF1	O9jjf1 mus musculus
40	20	4.5	631	11	O9JJF2	O9jjf2 mus musculus
41	18	4.0	497	11	O9WUJ0	O9wu0 mus musculus
42	15	3.3	44	6	O8WMO8	O8wmq8 canis famil
43	14	3.1	228	5	O27918	O27918 mya arenari
44	14	3.1	265	13	O9W681	O9w681 oncorhynch
45	14	3.1	265	13	O9W682	O9w682 oncorhynch

#### ALIGNMENTS

#### RESULT 1

Q9H3D2 ID Q9H3D2 PRELIMINARY: PRT: 487 AA.  
AC Q9H3D2; O76078;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE TA p63 gamma (P51 isoform TAP63GAMMA).  
GS P63.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98448095; PubMed=9774969;  
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,  
RA Andrews N.C., Caput D., McKee F.;  
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
RT transactivating, death-inducing, and dominant-negative activities.";  
RL Mol. Cell 2:305-316(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hagiwara K., McMenamin M.G., Harris C.C.;  
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 40-487 FROM N.A.  
RC TISSUE-SKELETAL MUSCLE;  
RX MEDLINE=98324755; PubMed=9662378;  
RA Osada M., Ohba M., Kawahara C., Ishloka C., Kanamaru R., Katoh I.,  
RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M., Ikawa S.;  
RT "Cloning and functional analysis of human p51, which structurally and  
RT functionally resembles p53.";  
RL Nat. Med. 4:839-843(1998).  
RN [4]  
RP SEQUENCE OF 40-487 FROM N.A.  
RX MEDLINE=20388515; PubMed=10935472;  
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,  
RA Yokota J.;

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RT "Mutation and expression of the p51 gene in human lung cancer.":
RL Neoplasia 1:71-79(1999).
DR EMBL; AF124540; AAG45609.1; -.
DR EMBL; AF124528; AAG45609.1; JOINED.
DR EMBL; AF124529; AAG45609.1; JOINED.
DR EMBL; AF124531; AAG45609.1; JOINED.
DR EMBL; AF124532; AAG45609.1; JOINED.
DR EMBL; AF124533; AAG45609.1; JOINED.
DR EMBL; AF124534; AAG45609.1; JOINED.
DR EMBL; AF124535; AAG45609.1; JOINED.
DR EMBL; AF075428; AAG62633.1; -.
DR EMBL; AB016072; BAA32592.1; -.
DR EMBL; AF116770; AAF43486.1; -.
DR EMBL; AF116756; AAF43486.1; JOINED.
DR EMBL; AF116757; AAF43486.1; JOINED.
DR EMBL; AF116759; AAF43486.1; JOINED.
DR EMBL; AF116760; AAF43486.1; JOINED.
DR EMBL; AF116761; AAF43486.1; JOINED.
DR EMBL; AF116762; AAF43486.1; JOINED.
DR EMBL; AF116763; AAF43486.1; JOINED.
DR EMBL; AF116764; AAF43486.1; JOINED.
DR EMBL; AF116765; AAF43486.1; JOINED.
DR HSSP; P04637; LYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 487 AA; 55687 MW; 86C863BDF2643DD CRC64;

Query Match          100.0%; Score 448; DB 4; Length 487;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 40 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
QY 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVWTPP 180
DB 160 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVWTPP 219
QY 181 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSLVYPPEPPQVGTFTTVLYNFMCSNCSVCGMNRRLIIVTLTRDQVGLGRRC 300
DB 280 ITGROSLVYPPEPPQVGTFTTVLYNFMCSNCSVCGMNRRLIIVTLTRDQVGLGRRC 339
QY 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 360
DB 340 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 399
QY 361 LLYLPVRGRETMYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQKLLSACFRNE 420
DB 400 LLYLPVRGRETMYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQKLLSACFRNE 459
QY 421 LVEPRRETQKQSDVFRHRSKPPNRSVYP 448
DB 460 LVEPRRETQKQSDVFRHRSKPPNRSVYP 487

RESULT 2
Q9NPH7
ID Q9NPH7 PRELIMINARY; PRT; 471 AA.
AC Q9NPH7
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

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DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE P51 isoform Tap63delta (P51 delta protein).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.":
RL Neoplasia 1:71-79(1999).
DR EMBL; AF116771; AAF61624.1; -.
DR EMBL; AF116769; AAF43489.1; JOINED.
DR EMBL; AF116756; AAF43489.1; JOINED.
DR EMBL; AF116757; AAF43489.1; JOINED.
DR EMBL; AF116759; AAF43489.1; JOINED.
DR EMBL; AF116760; AAF43489.1; JOINED.
DR EMBL; AF116761; AAF43489.1; JOINED.
DR EMBL; AF116762; AAF43489.1; JOINED.
DR EMBL; AF116763; AAF43489.1; JOINED.
DR EMBL; AF116764; AAF43489.1; JOINED.
DR EMBL; AF116765; AAF43489.1; JOINED.
DR HSSP; P04637; LYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 471 AA; 52882 MW; 32EB39798FC1CB69 CRC64;

Query Match          91.5%; Score 410; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSQSTQTNFLSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVWTPP 180
DB 121 SPSPAIPSTNDYPGPHSFQVDFVQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVWTPP 180
QY 181 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSLVYPPEPPQVGTFTTVLYNFMCSNCSVCGMNRRLIIVTLTRDQVGLGRRC 300
DB 241 ITGROSLVYPPEPPQVGTFTTVLYNFMCSNCSVCGMNRRLIIVTLTRDQVGLGRRC 300
QY 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 360
DB 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQIQTISIKRRSPDDE 360
QY 361 LLYLPVRGRETMYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQK 410
DB 361 LLYLPVRGRETMYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQK 410

RESULT 3
Q9P1B7
ID Q9P1B7 PRELIMINARY; PRT; 516 AA.
AC Q9P1B7
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

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DE P51 isoform Tap63beta.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20388515; PubMed=10935472;  
RA Tanl M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,  
RA Yokota J.  
RT "Mutation and expression of the p51 gene in human lung cancer."  
RL Neoplasia 1:71-79(1999).  
DR EMBL; AF116769; AAF43488.1; JOINED.  
DR EMBL; AF116756; AAF43488.1; JOINED.  
DR EMBL; AF116757; AAF43488.1; JOINED.  
DR EMBL; AF116759; AAF43488.1; JOINED.  
DR EMBL; AF116760; AAF43488.1; JOINED.  
DR EMBL; AF116761; AAF43488.1; JOINED.  
DR EMBL; AF116762; AAF43488.1; JOINED.  
DR EMBL; AF116763; AAF43488.1; JOINED.  
DR EMBL; AF116764; AAF43488.1; JOINED.  
DR EMBL; AF116765; AAF43488.1; JOINED.  
DR EMBL; AF116766; AAF43488.1; JOINED.  
DR EMBL; AF116767; AAF43488.1; JOINED.  
DR HSSP; P04637; IYCS.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; UNKNOWN\_1.  
SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;  
  
Query Match 91.5%; Score 410; DB 4; Length 516;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60  
DB 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60  
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
DB 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180  
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180  
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
DB 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
QY 241 ITGROSVLVPEPPQVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 300  
DB 241 ITGROSVLVPEPPQVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 300  
QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRSPDDE 360  
DB 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRSPDDE 360  
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 410  
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 410  
  
RESULT 4  
Q9H3D3 PRELIMINARY; PRT; 555 AA.  
AC Q9H3D3; Q9UP27;  
DT 01-MAR-2001 (TremBLrel. 16, Created)  
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)  
DE TA p63 beta.

GN P63.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98448095; PubMed=9774969;  
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,  
RA Andrews N.C., Caput D., McKeon F.  
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
RT transactivating, death-inducing, and dominant-negative activities."  
RL Mol. Cell 2:305-316(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hagihara K., McMenamin M.G., Harris C.C.;  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF124539; AAG45608.1; JOINED.  
DR EMBL; AF124528; AAG45608.1; JOINED.  
DR EMBL; AF124529; AAG45608.1; JOINED.  
DR EMBL; AF124531; AAG45608.1; JOINED.  
DR EMBL; AF124532; AAG45608.1; JOINED.  
DR EMBL; AF124533; AAG45608.1; JOINED.  
DR EMBL; AF124534; AAG45608.1; JOINED.  
DR EMBL; AF124535; AAG45608.1; JOINED.  
DR EMBL; AF124536; AAG45608.1; JOINED.  
DR EMBL; AF124537; AAG45608.1; JOINED.  
DR EMBL; AF075432; AAC62637.1; JOINED.  
DR HSSP; P04637; IYCS.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; UNKNOWN\_1.  
SQ SEQUENCE 555 AA; 62433 MW; E22874BE7DBABCBE CRC64;  
  
Query Match 91.5%; Score 410; DB 4; Length 555;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60  
DB 40 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99  
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
DB 100 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159  
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180  
DB 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219  
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
DB 220 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 279  
QY 241 ITGROSVLVPEPPQVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 300  
DB 280 ITGROSVLVPEPPQVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETROGQVLGRRC 339  
QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRSPDDE 360  
DB 340 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRSPDDE 399  
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 410  
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQK 449  
  
RESULT 5  
O75195 PRELIMINARY; PRT; 641 AA.  
ID O75195  
AC O75195;

DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE P51 isoform TAP63ALPHA (P51B protein).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SKELETAL MUSCLE;  
RX MEDLINE=98324755; PubMed=9662378;  
RA Osaka M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,  
RA Ikawa Y., Nimura Y., Nakagawa A., Obinata M.;  
RT "Cloning and functional analysis of human p51, which structurally and  
RT functionally resembles p53.";  
RL Nat. Med. 4:839-844(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20388515; PubMed=10935472;  
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,  
RA Yokota J.;  
RT "Mutation and expression of the p51 gene in human lung cancer.";  
RL Neoplasia 1:71-79(1999).  
DR EMBL; AB016073; BAA32593.1; -  
DR EMBL; AF116769; AAF43487.1; -  
DR EMBL; AF116756; AAF43487.1; JOINED.  
DR EMBL; AF116757; AAF43487.1; JOINED.  
DR EMBL; AF116759; AAF43487.1; JOINED.  
DR EMBL; AF116760; AAF43487.1; JOINED.  
DR EMBL; AF116761; AAF43487.1; JOINED.  
DR EMBL; AF116762; AAF43487.1; JOINED.  
DR EMBL; AF116763; AAF43487.1; JOINED.  
DR EMBL; AF116764; AAF43487.1; JOINED.  
DR EMBL; AF116765; AAF43487.1; JOINED.  
DR EMBL; AF116766; AAF43487.1; JOINED.  
DR EMBL; AF116767; AAF43487.1; JOINED.  
DR EMBL; AF116768; AAF43487.1; JOINED.  
DR HSSP; P04637; 1YCS.  
DR InterPro; IPR002117; P53.  
DR InterPro; IPR001660; SAM.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR SMART; SM00454; SAM; 1.  
DR PROSITE; PS00348; P53; UNKNOWN\_1.  
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;  
  
Query Match 91.5%; Score 410; DB 4; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MSQSTQTFNEFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIISMDCIQM 60  
DB 1 MSQSTQTFNEFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIISMDCIQM 60  
  
QY 61 DSDLSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 120  
DB 61 DSDLSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 120  
  
QY 121 SPSPALPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180  
DB 121 SPSPALPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180  
  
QY 181 PQGAVIRAMPYVYKAEHVTYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
DB 181 PQGAVIRAMPYVYKAEHVTYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
  
QY 241 ITGROSLVLPYEPPOVGTEFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 300  
DB 241 ITGROSLVLPYEPPOVGTEFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 300  
  
QY 301 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIIKKRRSPDDE 360

DB 301 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIIKKRRSPDDE 360  
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 410  
DB 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 410  
  
RESULT 6  
Q9UE10  
ID Q9UE10 PRELIMINARY; PRT; 680 AA.  
AC Q9UE10;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE KET protein.  
GN KET.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-SKELETAL MUSCLE AND KERATINOCYTE CULTURE;  
RX MEDLINE=99018225; PubMed=9799841;  
RA Augustin M., Bamberger C., Paul D., Schmale H.;  
RT "Cloning and chromosomal mapping of the human p53-related KET gene to  
RT chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.";  
RL Mamm. Genome 9:899-902(1998).  
DR EMBL; Y16961; CAA76562.1; -  
DR HSSP; P04637; 1YCS.  
DR InterPro; IPR002117; P53.  
DR InterPro; IPR001660; SAM.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR SMART; SM00454; SAM; 1.  
DR PROSITE; PS00348; P53; UNKNOWN\_1.  
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

Query Match 91.5%; Score 410; DB 4; Length 680;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MSQSTQTFNEFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIISMDCIQM 60  
DB 40 MSQSTQTFNEFLSPEVQFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKEIISMDCIQM 99  
  
QY 61 DSDLSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 120  
DB 100 DSDLSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTPSPYAPQPSSTFDAL 159  
  
QY 121 SPSPALPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180  
DB 160 SPSPALPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219  
  
QY 181 PQGAVIRAMPYVYKAEHVTYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240  
DB 220 PQGAVIRAMPYVYKAEHVTYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279  
  
QY 241 ITGROSLVLPYEPPOVGTEFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 300  
DB 280 ITGROSLVLPYEPPOVGTEFTVLNFMNCSSCVGGMNRRPILIIIVTLETRDQGVLRRC 339  
  
QY 301 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIIKKRRSPDDE 360  
DB 340 FEARICACGRDKADESIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIIKKRRSPDDE 399  
  
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 410  
DB 400 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTTETTRQOQQOQHLLQK 449



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Db      75 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
Qy      190 PVYKKAHEVTVVKRCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db      135 PVYKKAHEVTVVKRCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy      250 PYEPPOVGTETTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 309
Db      195 PYEPPOVGTETTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 254
Qy      310 GRDKADEDSIRKQVSDSTKNGDGTKRPRFRONTGHGQIOMTSIKKRRSPDDELLYLPVGR 369
Db      255 GRDKADEDSIRKQVSDSTKNGDGTKRPRFRONTGHGQIOMTSIKKRRSPDDELLYLPVGR 314
Qy      370 EYEMLLKIKESLELMQYLPOHTIETRYQQQQOHHLLQKHLLSACFRNELVPRRTEP 429
Db      315 EYEMLLKIKESLELMQYLPOHTIETRYQQQQOHHLLQKHLLSACFRNELVPRRTEP 374
Qy      430 KOSDVFFRHSKPPNRSVYP 448
Db      375 KOSDVFFRHSKPPNRSVYP 393

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## RESULT 9

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Q9P1B6
ID Q9P1B6 PRELIMINARY; PRT; 416 AA.
AC Q9P1B6
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE P51 isoform delNdelta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AF116769; AAF43493.1; JOINED.
DR EMBL; AF116758; AAF43493.1; JOINED.
DR EMBL; AF116759; AAF43493.1; JOINED.
DR EMBL; AF116760; AAF43493.1; JOINED.
DR EMBL; AF116761; AAF43493.1; JOINED.
DR EMBL; AF116762; AAF43493.1; JOINED.
DR EMBL; AF116763; AAF43493.1; JOINED.
DR EMBL; AF116764; AAF43493.1; JOINED.
DR EMBL; AF116765; AAF43493.1; JOINED.
DR EMBL; AF116766; AAF43493.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 416 AA; 46589 MW; A5974A14B25E3118 CRC64;

```

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Query Match      76.1%; Score 341; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
Db      15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
Qy      130 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db      75 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134

```

```

Qy      190 PVYKKAHEVTVVKRCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db      135 PVYKKAHEVTVVKRCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy      250 PYEPPOVGTETTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 309
Db      195 PYEPPOVGTETTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 254
Qy      310 GRDKADEDSIRKQVSDSTKNGDGTKRPRFRONTGHGQIOMTSIKKRRSPDDELLYLPVGR 369
Db      255 GRDKADEDSIRKQVSDSTKNGDGTKRPRFRONTGHGQIOMTSIKKRRSPDDELLYLPVGR 314
Qy      370 EYEMLLKIKESLELMQYLPOHTIETRYQQQQOHHLLQK 410
Db      315 EYEMLLKIKESLELMQYLPOHTIETRYQQQQOHHLLQK 355

```

## RESULT 10

```

Q9P1B5
ID Q9P1B5 PRELIMINARY; PRT; 461 AA.
AC Q9P1B5
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE P51 isoform delNbeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AF116769; AAF43492.1; JOINED.
DR EMBL; AF116758; AAF43492.1; JOINED.
DR EMBL; AF116759; AAF43492.1; JOINED.
DR EMBL; AF116760; AAF43492.1; JOINED.
DR EMBL; AF116761; AAF43492.1; JOINED.
DR EMBL; AF116762; AAF43492.1; JOINED.
DR EMBL; AF116763; AAF43492.1; JOINED.
DR EMBL; AF116764; AAF43492.1; JOINED.
DR EMBL; AF116765; AAF43492.1; JOINED.
DR EMBL; AF116766; AAF43492.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 461 AA; 51305 MW; 68B63547B81C1B05 CRC64;

```

```

Query Match      76.1%; Score 341; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
Db      15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
Qy      130 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db      75 TDTPGPHSFVDSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
Qy      190 PVYKKAHEVTVVKRCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db      135 PVYKKAHEVTVVKRCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy      250 PYEPPOVGTETTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 309

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```
Db 195 PYEPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
Qy 310 GRDKADEDSIRKQVSDSTKNGDGTTRPPRQNTGHGIQMTSIRKRRSPDDELLYLPVGR 369
Db 255 GRDKADEDSIRKQVSDSTKNGDGTTRPPRQNTGHGIQMTSIRKRRSPDDELLYLPVGR 314
Qy 370 ETYEMLLKIKESLELMQYLPQHTIETTRQOQQOQHLLQK 410
Db 315 ETYEMLLKIKESLELMQYLPQHTIETTRQOQQOQHLLQK 355

RESULT 11
Q9UP26 PRELIMINARY; PRT; 461 AA.
ID Q9UP26
AC Q9UP26
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DN P63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang X., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagihara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075433; AAC62638.1; -.
DR EMBL; AF124539; AAG45611.1; JOINED.
DR EMBL; AF124530; AAG45611.1; JOINED.
DR EMBL; AF124531; AAG45611.1; JOINED.
DR EMBL; AF124532; AAG45611.1; JOINED.
DR EMBL; AF124533; AAG45611.1; JOINED.
DR EMBL; AF124534; AAG45611.1; JOINED.
DR EMBL; AF124535; AAG45611.1; JOINED.
DR EMBL; AF124536; AAG45611.1; JOINED.
DR EMBL; AF124537; AAG45611.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;

Query Match 76.1%; Score 341; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
Db 15 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
Qy 130 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db 75 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
Qy 190 PVYKKAHVTEVVKRCNHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 75 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
Qy 190 PVYKKAHVTEVVKRCNHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCNHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy 250 PYEPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 309
Db 195 PYEPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
Qy 195 PYEPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
Db 195 PYEPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
```

```
Qy 310 GRDKADEDSIRKQVSDSTKNGDGTTRPPRQNTGHGIQMTSIRKRRSPDDELLYLPVGR 369
Db 255 GRDKADEDSIRKQVSDSTKNGDGTTRPPRQNTGHGIQMTSIRKRRSPDDELLYLPVGR 314
Qy 370 ETYEMLLKIKESLELMQYLPQHTIETTRQOQQOQHLLQK 410
Db 315 ETYEMLLKIKESLELMQYLPQHTIETTRQOQQOQHLLQK 355

RESULT 12
Q9P1B4 PRELIMINARY; PRT; 586 AA.
ID Q9P1B4
AC Q9P1B4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P51 isoform delNalpa.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL; AF116769; AAF43491.1; -.
DR EMBL; AF116758; AAF43491.1; JOINED.
DR EMBL; AF116759; AAF43491.1; JOINED.
DR EMBL; AF116760; AAF43491.1; JOINED.
DR EMBL; AF116761; AAF43491.1; JOINED.
DR EMBL; AF116762; AAF43491.1; JOINED.
DR EMBL; AF116763; AAF43491.1; JOINED.
DR EMBL; AF116764; AAF43491.1; JOINED.
DR EMBL; AF116765; AAF43491.1; JOINED.
DR EMBL; AF116766; AAF43491.1; JOINED.
DR EMBL; AF116767; AAF43491.1; JOINED.
DR EMBL; AF116768; AAF43491.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 76.1%; Score 341; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
Db 15 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
Qy 130 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db 75 TDYPGHSDVDFVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
Qy 190 PVYKKAHVTEVVKRCNHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCNHELSEFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
Qy 250 PYEPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 309
Db 195 PYEPQVGTETTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVILGRRCFEARICACP 254
Qy 310 GRDKADEDSIRKQVSDSTKNGDGTTRPPRQNTGHGIQMTSIRKRRSPDDELLYLPVGR 369
Db 255 GRDKADEDSIRKQVSDSTKNGDGTTRPPRQNTGHGIQMTSIRKRRSPDDELLYLPVGR 314
```

```
Db 255 GRDRKADEDSIRKQOVSSTKNGDCTKRPRQNTHTGIQMTSIKKRSPPDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQK 410
Db 315 EYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQK 355

RESULT 13
Q9UBV9
ID Q9UBV9 PRELIMINARY; PRT; 586 AA.
AC Q9UBV9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE DN P63 alpha.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
RT Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
Dellavalle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
Jablonska S.;
RT "Characterization of an autoantigen associated with chronic ulcerative
stomatitis: The CUSP autoantigen is a member of the p53 family.";
RT J. Invest. Dermatol. 0:0-0(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Hagihara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075431; AAC62636.1; -
DR EMBL; AF091627; AAC43038.1; -
DR EMBL; AF124539; AAG45610.1; -
DR EMBL; AF124530; AAG45610.1; JOINED.
DR EMBL; AF124531; AAG45610.1; JOINED.
DR EMBL; AF124532; AAG45610.1; JOINED.
DR EMBL; AF124533; AAG45610.1; JOINED.
DR EMBL; AF124534; AAG45610.1; JOINED.
DR EMBL; AF124535; AAG45610.1; JOINED.
DR EMBL; AF124536; AAG45610.1; JOINED.
DR EMBL; AF124537; AAG45610.1; JOINED.
DR EMBL; AF124538; AAG45610.1; JOINED.
DR HSSP; P04637; LYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001650; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 586 AA; 65756 MW; 2E2F92ABF1AF8629 CRC64;

Query Match 76.1%; Score 341; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PONTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQSSSTFDALSPSPAFPSN 129
Db 15 PONTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQSSSTFDALSPSPAFPSN 74

QY 130 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYLCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db 75 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYLCQIAKTCPIQIKVMTPPQGAIVRAM 134
```

```
QY 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPQVGTETFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDQGVLRRCFEARICACP 309
Db 195 PYEPPQVGTETFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDQGVLRRCFEARICACP 254
QY 310 GRDRKADEDSIRKQOVSSTKNGDCTKRPRQNTHTGIQMTSIKKRSPPDELLYLPVGR 369
Db 255 GRDRKADEDSIRKQOVSSTKNGDCTKRPRQNTHTGIQMTSIKKRSPPDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQK 410
Db 315 EYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQK 355
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## RESULT 14

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O88897
ID O88897 PRELIMINARY; PRT; 483 AA.
AC O88897;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE TA*p63 gamma.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
DR EMBL; AF075434; AAC62639.1; -
DR HSSP; P04637; LYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 483 AA; 54969 MW; A90E0DC110C50EAD CRC64;
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Query Match 63.4%; Score 284; DB 11; Length 483;
Best Local Similarity 100.0%; Pred. No. 7;le=290;
Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GATNKKIELSMDCIRMQSDLSLSDPMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSV 104
Db 84 GATNKKIELSMDCIRMQSDLSLSDPMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSV 143
QY 105 TAPSPYAPSSSTFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYC 164
Db 144 TAPSPYAPSSSTFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYC 203
QY 165 QIAKTCPIQIKVMTPPQGAIVRAMPYVKKAEHVTEVVKRCPNHLSREFNEGQIAPPSh 224
Db 204 QIAKTCPIQIKVMTPPQGAIVRAMPYVKKAEHVTEVVKRCPNHLSREFNEGQIAPPSh 263
QY 225 LIRVEGNSHAQYVEDPITGRQSVLVYEPPOVGTETFTVLYNFMCMNSCVGGMNRRPILI 284
Db 264 LIRVEGNSHAQYVEDPITGRQSVLVYEPPOVGTETFTVLYNFMCMNSCVGGMNRRPILI 323
QY 285 IVTLETRDQGVLRRCFEARICACPGDRKADEDSIRKQOVS 328
Db 324 IVTLETRDQGVLRRCFEARICACPGDRKADEDSIRKQOVS 367
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```
RESULT 15
Q9QWZ0
ID Q9QWZ0 PRELIMINARY; PRT; 555 AA.
AC Q9QWZ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TA*p63 beta.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., Mckeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
DR EMBL; AF075435; AAC62640.1; -.
DR HSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ SEQUENCE 555 AA; 62454 MW; 059E034046EB8987 CRC64;

Query Match 63.4%; Score 284; DB 11; Length 555;
Best Local Similarity 100.0%; Pred. No. 8e-290;
Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 GATNKIEISDCIRMQDSDLSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSV 104
Db 84 GATNKIEISDCIRMQDSDLSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSV 143
Qy 105 TAPSPYAQPSTFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYC 164
Db 144 TAPSPYAQPSTFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYC 203
Qy 165 QIAKTCPIQIKVMTPPQGAIVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGQIAPPSH 224
Db 204 QIAKTCPIQIKVMTPPQGAIVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGQIAPPSH 263
Qy 225 LIRVEGNSHAQYVEDPITGRQSVLVYPYEPQVGTEFTVLYNFMCSNCSVGGMNRRLI 284
Db 264 LIRVEGNSHAQYVEDPITGRQSVLVYPYEPQVGTEFTVLYNFMCSNCSVGGMNRRLI 323
Qy 285 IVLETRDGVLRRCFEARICACPGDRKADEDSIRKQVSDS 328
Db 324 IVLETRDGVLRRCFEARICACPGDRKADEDSIRKQVSDS 367

Search completed: June 24, 2003, 22:25:04
Job time : 38 secs
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:19:31 ; Search time 15 Seconds  
(without alignments)  
1238.760 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 448

Sequence: 1 MSQSTQTNFLSPEVFOHIW.....PKQSDVFRHSPKPNRSVYP 448

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	4.9	636	1 P73_HUMAN	O15350 homo sapien
2	22	4.9	637	1 P73_CERAE	Q9XSK8 cercopithec
3	15	3.3	369	1 P53_BARBU	Q9W678 barbus barb
4	13	2.9	367	1 P53_CHICK	P10360 gallus gall
5	13	2.9	396	1 P53_ONCYA	P25035 oncorhynchu
6	11	2.5	352	1 P53_ORYLA	P79820 oryzias lat
7	10	2.2	393	1 P53_CRIGR	Q09185 cricetus
8	10	2.2	393	1 P53_TUPGB	Q9TCAI tupaia glis
9	10	2.2	396	1 P53_MESAU	Q00366 mesocricetu
10	9	2.0	195	1 HUNB_DRODA	O46262 drosophila
11	9	2.0	196	1 HUNB_DROAA	O46234 drosophila
12	9	2.0	201	1 AST5_DROME	P10083 drosophila
13	9	2.0	207	1 P53_EQVAS	Q29480 equus asinu
14	9	2.0	280	1 P53_HORSE	P79892 equus caball
15	9	2.0	314	1 P53_SPEBE	O64662 spermophilu
16	9	2.0	342	1 P53_XIPHE	O57538 xiphophorus
17	9	2.0	342	1 P53_XIPMA	Q92143 xiphophorus
18	9	2.0	363	1 P53_XENLA	P07193 xenopus lae
19	9	2.0	366	1 P53_PLAFE	O12346 platichthys
20	9	2.0	367	1 P53_TETMU	Q9W679 tetraodon m
21	9	2.0	373	1 P53_BRARE	P79734 brachyodon m
22	9	2.0	376	1 P53_ICTPU	O93379 ictalurus p
23	9	2.0	381	1 P53_CANFA	Q29537 canis famil
24	9	2.0	382	1 P53_SHEEP	P51664 ovis aries
25	9	2.0	386	1 P53_BOVIN	Q29628 bos taurus
26	9	2.0	386	1 P53_FELCA	P41685 felis silve
27	9	2.0	386	1 P53_PIG	Q9TUB2 sus scrofa
28	9	2.0	390	1 P53_MOUSE	P02340 mus musculu
29	9	2.0	391	1 P53_CAVPO	Q9WUR6 cavla porce
30	9	2.0	391	1 P53_MARMO	O36006 marmota mon
31	9	2.0	391	1 P53_RABIT	Q95330 coryctolagus
32	9	2.0	391	1 P53_RAT	P10361 rattus norv
33	9	2.0	393	1 P53_CERAE	P13481 cercopithec

## RESULT 1

ID	P73_HUMAN	STANDARD;	PRT;	636 AA.
AC	O15350; O15351; Q9NTRK8;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).			
DE	TP73 OR P73.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).			
RC	TISSUE=Colon;			
RX	MEDLINE=97433090; PubMed=9288759;			
RA	Raghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., Minty A., Chalou P., Lelias J.-M., Dumont X., Ferrara P., McKeon F., Caput D.;			
RT	"Monoclonally expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers."			
RL	Cell 90:809-819(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=99289209; PubMed=10362363;			
RA	Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K., Harris C.C.;			
RT	"Mutational analysis of p73 and p53 in human cancer cell lines."			
RL	Oncogene 18:3415-3421(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=98389621; PubMed=9721206;			
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.;			
RT	"Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions."			
RL	Genomics 51:359-363(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).			
RC	TISSUE=Neuroblastoma;			
RX	MEDLINE=99021697; PubMed=9802988;			
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Annicchiarico-Petruzzelli M., Leviero M., Melino G.;			
RT	"Two new p73 splice variants, gamma and delta, with different transcriptional activity."			
RL	J. Exp. Med. 188:1763-1768(1998).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).			
RC	TISSUE=Lymphocytes, Breast Cancer, Hepatoma, and Skin;			
RX	MEDLINE=99310938; PubMed=10381648;			
RA	De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Leviero M., Knight R.A.;			
RT	"Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splice variants epsilon and zeta."			

34	9	2.0	393	1 P53_HUMAN	P04637 homo sapien
35	9	2.0	393	1 P53_MACFA	P56423 macaca fasc
36	9	2.0	393	1 P53_MACMU	P56424 macaca mula
37	9	2.0	481	1 KNIR_DROVI	Q24753 drosophila
38	9	2.0	635	1 HMLA_DROME	P10105 drosophila
39	9	2.0	816	1 ATXI_HUMAN	P54253 homo sapien
40	9	2.0	1167	1 WCI_NEUCR	Q01371 neurospora
41	9	2.0	1394	1 E75B_DROME	P17672 drosophila
42	8	1.8	54	1 SASG_BACFI	P35142 saccharomyc
43	8	1.8	150	1 CKS1_YEAST	P20486 saccharomyc
44	8	1.8	170	1 VIMI_CARAU	P48671 carassius a
45	8	1.8	192	1 HUNB_DROAD	O46232 drosophila

## ALIGNMENTS

Cell Death Differ. 6:389-390(1999).  
 [6] SEQUENCE FROM N.A. (ISOFORM KAPPA).  
 RA Thomas D.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=99318135; PubMed=10391251;  
 RA Kharbada S., Shiroya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response  
 to DNA damage";  
 RL Nature 399:814-817(1999).  
 RN [8]  
 RP ERRATUM.  
 RA Yuan Z.-M., Shiroya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RL Kharbada S., Weichselbaum R., Kufe D.;  
 RN Nature 400:792-792(1999).  
 RP [9]  
 RP FUNCTION.  
 RX MEDLINE=99217940; PubMed=10203277;  
 RA Kaelin W.G. Jr.;  
 RT "The emerging p53 gene family";  
 RL J. Natl. Cancer Inst. 91:594-598(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 439-506.  
 RX MEDLINE=99380160; PubMed=10449409;  
 RA Chl S.W., Ayed A., Arrowsmith C.H.;  
 RT "Solution structure of a conserved C-terminal domain of p73 with  
 structural homology to the SAM domain";  
 RL EMBO J. 18:4438-4445(1999).  
 CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.  
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE  
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR  
 CC PROTEIN.  
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL  
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY  
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA  
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA  
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: 7 ISOFORMS; ALPHA (SHOWN HERE), BETA, GAMMA,  
 CC DELTA, EPSILON, ZETA AND KAPPA; ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING. THE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS  
 CC RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE  
 CC SPLICING OF EXON 13 IN EPSILON ISOFORM REVERTS THE READING FRAME  
 CC TO THE ALPHA ISOFORM.  
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,  
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.  
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.  
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN. A CENTRAL DNA  
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS  
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.  
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE  
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED  
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN  
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; Y11416; CAAT72220.1; -  
 DR EMBL; Y11416; CAAT72221.1; -  
 DR EMBL; Y11416; CAAT72219.1; -  
 DR EMBL; AF077628; AAC61887.1; -  
 DR EMBL; AF077616; AAC61887.1; JOINED.  
 DR EMBL; AF077617; AAC61887.1; JOINED.

DR EMBL; AF077618; AAC61887.1; JOINED.  
 DR EMBL; AF077619; AAC61887.1; JOINED.  
 DR EMBL; AF077620; AAC61887.1; JOINED.  
 DR EMBL; AF077621; AAC61887.1; JOINED.  
 DR EMBL; AF077622; AAC61887.1; JOINED.  
 DR EMBL; AF077623; AAC61887.1; JOINED.  
 DR EMBL; AF077624; AAC61887.1; JOINED.  
 DR EMBL; AF077625; AAC61887.1; JOINED.  
 DR EMBL; AF077626; AAC61887.1; JOINED.  
 DR EMBL; AF077627; AAC61887.1; JOINED.  
 DR EMBL; AF079094; AAC39696.1; -  
 DR EMBL; AF079082; AAD39696.1; JOINED.  
 DR EMBL; AF079083; AAD39696.1; JOINED.  
 DR EMBL; AF079084; AAD39696.1; JOINED.  
 DR EMBL; AF079085; AAD39696.1; JOINED.  
 DR EMBL; AF079086; AAD39696.1; JOINED.  
 DR EMBL; AF079087; AAD39696.1; JOINED.  
 DR EMBL; AF079088; AAD39696.1; JOINED.  
 DR EMBL; AF079089; AAD39696.1; JOINED.  
 DR EMBL; AF079090; AAD39696.1; JOINED.  
 DR EMBL; AF079091; AAD39696.1; JOINED.  
 DR EMBL; AF079092; AAD39696.1; JOINED.  
 DR EMBL; AF079093; AAD39696.1; JOINED.  
 DR EMBL; ALI36528; CAB92742.1; -  
 DR PDB; 1COK; 17-AUG-99.  
 DR TRANSFAC; T04931; -  
 DR Genew; HGNC:12003; TP73.  
 DR MIM; 601990; -  
 DR InterPro; IPR002117; P53.  
 DR InterPro; IPR001660; SAM.  
 DR Pfam; PF00536; SAM; 1.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSOR.  
 DR ProDom; PD002681; P53; 1.  
 DR SMART; SM00454; SAM; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;  
 KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;  
 KW 3D-structure.  
 FT DOMAIN 1 46  
 FT DOMAIN 1 55  
 FT DOMAIN 287 304  
 FT DOMAIN 346 435  
 FT DOMAIN 168 171  
 FT DOMAIN 391 394  
 FT DOMAIN 483 486  
 FT DOMAIN 131 310  
 FT MOD\_RES 99 99  
 FT VARSPLIC 282 282  
 FT VARSPLIC 495 636  
 FT VARSPLIC 400 476  
 FT VARSPLIC 477 636  
 FT VARSPLIC 400 403  
 FT VARSPLIC 404 636  
 FT VARSPLIC 400 445  
 FT VARSPLIC 446 526  
 FT VARSPLIC 400 495  
 FT SEQUENCE 636 AA; 69623 MW; A467493C5D93EE0 CRC64;  
 Query Match 4.9%; Score 22; DB 1; Length 636;  
 Best Local Similarity 100.0%; Pred. No. 5,2e-14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 264 LYFMCNCSVCGVMRRPILII 285

Db 253 LYNECMSSCVGMNRRPILII 274  
|||||

## RESULT 2

P73\_CERAE STANDARD; PRT; 637 AA.  
AC Q9XSK8; Q9TSQ9;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).  
GN TP73 OR P73.  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Caput D.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE. WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN (BY SIMILARITY).  
CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; Y11419; CAA72224.1; -;  
DR EMBL; Y11419; CAA72225.1; -;  
DR HSSP; O15350; ICKO.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00536; SAM; 1.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR SMART; SM00454; SAM; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.  
FT VARSPPLIC 495 637  
FT SFTLGLGCPNCIEFTSOGLOSIVHLQNTIEDLGALKIPE  
FT QYRMTIWRGLQDLKQGHYGAQAQLRSSNAIAISIGSG  
FT ELQRYVMEAVHFRVHTITIPNRGGPGAGDEWADFGDL  
FT PCKARKQPIKEEFTAEIHF -> RTWGP (IN ISOFORM BETA).  
SQ SEQUENCE 637 AA; 69630 MW; 7CB20B919C9C70A CRC64;

Query Match 4.9%; Score 22; DB 1; Length 637;  
Best Local Similarity 100.0%; Pred. No. 5.2e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 LYNECMSSCVGMNRRPILII 285  
|||||

Db 253 LYNECMSSCVGMNRRPILII 274

## RESULT 3

P53\_BARBU STANDARD; PRT; 369 AA.  
AC Q9W678;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53 OR P53.  
OS Barbus barbus (Barbel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Barbus.  
OX NCBI\_TaxID=40830;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;  
RT "Evolutionary conservancy of p53 gene sequences in fish."  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; Induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).  
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; AF071570; AAD34212.1; -;  
DR HSSP; P04637; ITUP.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 28  
FT DNA\_BIND 66 256  
FT DOMAIN 298 329  
FT DOMAIN 342 365  
FT DOMAIN 276 292  
FT MOD\_RES 368 368  
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEA74C304 CRC64;

Query Match 3.3%; Score 15; DB 1; Length 369;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 EFTTVLYNFMNNSC 273  
|||||

Db 192 EFTTVLYNFMNNSC 206  
|||||

## RESULT 4

P53\_CHICK STANDARD; PRT; 367 AA.  
ID P53\_CHICK  
AC P10360;

DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53.  
 OS Gallus gallus (Chicken).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPAFS;  
 RX MEDLINE=89083584; PubMed=3060861;  
 RA Soussi T.;  
 RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear  
 oncoprotein.";  
 RL Nucleic Acids Res. 16:11383-11383(1988).  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 growth arrest or apoptosis depending on the physiological  
 circumstances and cell type. Involved in cell cycle regulation as  
 a trans-activator that acts to negatively regulate cell division  
 by controlling a set of genes required for this process. One of  
 the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 BAX and FAS antigen expression, or by repression of Bcl-2  
 expression (By similarity).  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL; X13057; CAA31456.1; -  
 DR PIR; S02193; S02193.  
 DR HSSP; P04637; ITUP.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA\_BIND 87 278 BY SIMILARITY.  
 FT DOMAIN 308 339 OLIGOMERIZATION.  
 FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 292 305 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 367 AA; 40169 MW; FC37D0FCDF915B6 CRC64;  
 Query Match 2.9%; Score 13; DB 1; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 261 TTVLYNFCMNCSSC 273  
 Db 216 TTVLYNFCMNCSSC 228  
 RESULT 5  
 ID P53\_ONCMY STANDARD; PRT; 396 AA.  
 AC P25035;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OC NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92210006; PubMed=1339362;  
 RA de Fromental C.C.; Packel F.; Chapus A.; Baney C.; May P.; Soussi T.;  
 RT "Rainbow trout p53: cDNA cloning and biochemical characterization.";  
 RL Gene 112:241-245(1992).  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 growth arrest or apoptosis depending on the physiological  
 circumstances and cell type. Involved in cell cycle regulation as  
 a trans-activator that acts to negatively regulate cell division  
 by controlling a set of genes required for this process. One of  
 the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 BAX and FAS antigen expression, or by repression of Bcl-2  
 expression (By similarity).  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL; M75145; AAA49605.1; -  
 DR PIR; JH0631; JH0631.  
 DR HSSP; P04637; ITUP.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA\_BIND 90 281 BY SIMILARITY.  
 FT DOMAIN 325 356 OLIGOMERIZATION.  
 FT DOMAIN 369 392 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 396 AA; 43966 MW; 8422250765545A1C CRC64;  
 Query Match 2.9%; Score 13; DB 1; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 261 TTVLYNFCMNCSSC 273  
 Db 219 TTVLYNFCMNCSSC 231  
 RESULT 6  
 ID P53\_ORYLA STANDARD; PRT; 352 AA.  
 AC P79820; Q9PSU7; Q9PSU8;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53 OR P53.  
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

CC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 CC Nebliniformes; Adrianchthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=97305153; PubMed=9161419;  
 RA Krause M.K., Rhodes L.D., van Beneden R.J.;  
 RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka  
 RT (Oryzias latipes) and evaluation of mutational hotspots in MNG-  
 RT exposed fish";  
 RL Gene 189:101-106(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT THR-91.  
 RC STRAIN=Himedaka;  
 RA Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;  
 RT "Isolation of cDNAs encoding the p53 tumor suppressor gene in the  
 RT Japanese Medaka (Oryzias latipes).";  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; Induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation  
 CC as a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression (By similarity).  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC  
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 CC  
 CC EMBL: U57306; AAC60146.1; -;  
 CC EMBL: AF003949; AAD01195.1; -;  
 CC EMBL: AF003950; AAD01196.1; -;  
 CC HSSP: P04637; 1YCS.  
 CC InterPro: IPR002117; P53.  
 CC Pfam: PF00870; P53; 1.  
 CC PRINTS: PR00386; P53SUPPRESSR.  
 CC PRODOM: PD002681; P53; 1.  
 CC PROSITE: PS00348; P53; 1.  
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.  
 FT DOMAIN 1 48  
 FT DNA\_BIND 87 273  
 FT DOMAIN 302 331  
 FT DOMAIN 334 350  
 FT DOMAIN 383 295  
 FT MOD\_RES 351 91  
 FT VARIANT 91 91  
 FT CONFLICT 22 22  
 SQ SEQUENCE 352 AA; 39753 MW; 196868A66351BFF5 CRC64;  
 Query Match 2.5%; Score 11; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 0.0038;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 304 RICACPGDRK 314  
 DB 254 RICACPGDRK 264  
 RESULT 7  
 ID P53\_CRIGR STANDARD; PRT; 393 AA.

AC 009185; Q64397; P97258; P97788;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53 OR P53.  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus  
 OX NCBI\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chaung W., Mi L.J., Boorstein R.J.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=97183659; PubMed=9031625;  
 RA Lee H., Lerner J.M., Hamlin J.L.;  
 RT "Cloning and characterization of Chinese hamster p53 cDNA.";  
 RL Gene 184:177-183(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic fibroblast;  
 RA Shimizu T., Nikaudo O., Suzuki F.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; Induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression.  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: Y08900; CAA70108.1; -;  
 CC EMBL: Y08901; CAA70109.1; -;  
 CC EMBL: U50395; AAC53040.1; -;  
 CC EMBL: D86070; BAAL3004.1; -;  
 CC HSSP: P04637; 1TUP.  
 CC InterPro: IPR002117; P53.  
 CC Pfam: PF00870; P53; 1.  
 CC PRINTS: PR00386; P53SUPPRESSR.  
 CC PRODOM: PD002681; P53; 1.  
 CC PROSITE: PS00348; P53; 1.  
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 45  
 FT DNA\_BIND 102 292  
 FT DOMAIN 325 356  
 FT DOMAIN 368 387  
 FT DOMAIN 311 323  
 FT MOD\_RES 392 392  
 FT VARIANT 133 133  
 FT VARIANT 135 135  
 FT CONFLICT 103 103  
 FT CONFLICT 103 103  
 SQ SEQUENCE 393 AA; 43378 MW; 2A7830E788311689 CRC64;

## Query Match

Best Local Similarity 2.2%; Score 10; DB 1; Length 393;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313  
Db 273 RICACPGDR 282

## RESULT 8

ID P53\_TUPGB STANDARD; PRT; 393 AA.  
AC O9TAL;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53 OR P53.  
OS Tupala gliis belangeri (Common tree shrew).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Scandentia; Tupalidae; Tupala.  
OX NCBI\_TaxID=9396;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Chinensis; TISSUE=Liver;  
RA Park U., Lee Y.;  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.  
-1- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
-1- SUBCELLULAR LOCATION: Nuclear.  
-1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.  
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; AF175893; AAF22640.1; -  
DR HSSP; P04637; IYCS.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR ProDom; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNA\_BIND 102 292 BY SIMILARITY.  
FT DOMAIN 325 356 OLIGOMERIZATION.  
FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;

## Query Match

Best Local Similarity 2.2%; Score 10; DB 1; Length 393;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313  
Db 273 RICACPGDR 282

## RESULT 9

ID P53\_MESAU STANDARD; PRT; 396 AA.  
AC Q00366; P97276;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OX Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Syrian; TISSUE=Kidney;  
RA MEDLINE=92210007; PubMed=1555773;  
RA Legros Y., McIntyre P., Soussi T.;  
RL "The cDNA cloning and immunological characterization of hamster p53.";  
RL Gene 112:247-250(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hou E.W., Wiseman R.;  
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.  
-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.  
-1- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
-1- SUBCELLULAR LOCATION: Nuclear.  
-1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.  
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; M75144; AAA37085.1; -  
DR EMBL; U07182; AAB41344.1; -  
DR PIR; JH0633; JH0633.  
DR HSSP; P04637; ITUP.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR ProDom; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNA\_BIND 105 295 BY SIMILARITY.  
FT DOMAIN 328 359 OLIGOMERIZATION.  
FT DOMAIN 371 390 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 314 326 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).  
FT CONFLICT 186 188 G -> S (IN REF. 2).

SQ SEQUENCE 396 AA; 43631 MW; 906F02568099BE3 CRC64;

Query Match 2.2%; Score 10; DB 1; Length 396;

Best Local Similarity 100.0%; Pred. No. 0.043; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313

|||||

Db 276 RICACPGDR 285

#### RESULT 10

HUNB\_DROAA

ID HUNB\_DROAA STANDARD; PRT; 195 AA.

AC O46262; 046263;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hunchback protein (Fragments).

GN HB.

OS Drosophila dasycnemia (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=58308;

[1]

RP SEQUENCE FROM N.A.

RA Baker R.H., Desalle R.;

RT "Multiple sources of character information and the phylogeny of

RT Hawaiian drosophilids."

RL Syst. Biol. 46:654-673(1997).

CC -!- FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT

CC OF HEAD STRUCTURES (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-

CC FINGER PROTEINS.

CC -----

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CC -----

DR EMBL; U93026; AAC03274.1; -.

DR EMBL; U93027; AAC03275.1; -.

DR FlyBase; FBgn0024069; Ddaas\hb.

KW Developmental protein; Gap protein; Zinc-finger;

KW Metal-binding; DNA-binding; Repeat; Nuclear protein.

FT NON\_TER 1

FT DOMAIN 17 29 POLY-HIS.

FT NON\_CONS 66 81 POLY-GLN.

FT DOMAIN 102 103

FT DOMAIN 130 136 POLY-ALA.

FT NON\_TER 195 195

SQ SEQUENCE 195 AA; 21335 MW; 4DA02122E1532AC3 CRC64;

Query Match

Best Local Similarity 2.0%; Score 9; DB 1; Length 195;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 OQOQOQH 406

|||||

Db 68 OQOQOQH 76

#### RESULT 11

HUNB\_DROAA

ID HUNB\_DROAA STANDARD; PRT; 196 AA.

AC O46234; 046235;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hunchback protein (Fragments).

GN HB.

OS Drosophila adunca (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=46893;

[1]

RP SEQUENCE FROM N.A.

RA Baker R.H., Desalle R.;

RT "Multiple sources of character information and the phylogeny of

RT Hawaiian drosophilids."

RL Syst. Biol. 46:654-673(1997).

CC -!- FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT

CC OF HEAD STRUCTURES (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-

CC FINGER PROTEINS.

CC -----

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CC -----

DR EMBL; U92998; AAC03247.1; -.

DR EMBL; U92999; AAC03246.1; -.

DR FlyBase; FBgn0024132; Dadu\hb.

KW Developmental protein; Gap protein; Zinc-finger;

KW Metal-binding; DNA-binding; Repeat; Nuclear protein.

FT NON\_TER 1

FT DOMAIN 17 29 POLY-HIS.

FT DOMAIN 65 80 POLY-GLN.

FT NON\_CONS 101 102

FT NON\_TER 196 196

SQ SEQUENCE 196 AA; 21683 MW; F961D7184FFE4C6F CRC64;

Query Match

Best Local Similarity 2.0%; Score 9; DB 1; Length 196;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 OQOQOQH 406

|||||

Db 67 OQOQOQH 75

#### RESULT 12

AST5\_DROME

ID AST5\_DROME STANDARD; PRT; 201 AA.

AC P10083; Q9W5G4;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Achaete-scute complex protein T5 (Achaete).

GN AC OR T5 OR EG:125H10.3 OR CG3796.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN-Canton-S;

RX MEDLINE=87273503; PubMed=3111716;

RA Villares R., Cabrera C.V.;

RT "The achaete-scute gene complex of D. melanogaster: conserved domains

RT in a subset of genes required for neurogenesis and their homology to

RL myc.";

RL Cell 50:415-424(1987).

[2]



SEQUENCE FROM N.A.  
 RA STRAIN-Oregon-R;  
 RX MEDLINE=20196011; PubMed=10731137;  
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,  
 RA Mirano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,  
 RA Papagiannakis G., Spanos L., Cox S., Siden-Klamos E., Bolshakov S.,  
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,  
 RA Belnert N., Dowe G., Schaefer U., Jacek H., Bucheton A.,  
 RA Callister D.M., Campbell L.A., Darlamsiton N.S.,  
 RA McMillan P.J., Sallies C., Tait E.A., Valenti P., Saunders R.D.C.,  
 RA Glover D.M.;  
 RT "From sequence to chromosome: the tip of the x chromosome of D.  
 RT melanogaster";  
 RL Science 287:2220-2222(2000).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RP STRAIN-Berkeley;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
 RA Mount S.D., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Wellenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: AS-C PROTEINS ARE INVOLVED IN THE DETERMINATION OF THE  
 CC NEURONAL PRECURSORS IN THE PERIPHERAL NERVOUS SYSTEM AND THE  
 CC CENTRAL NERVOUS SYSTEM.  
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER  
 CC BHLH PROTEIN.  
 CC TISSUE SPECIFICITY: L(1)SC, SC AND AC STRONGLY LABEL THE  
 CC PRESUMPTIVE STOMATOGASTRIC NERVOUS SYSTEM, WHILE ASE IS MORE  
 CC PROMINENT IN THE PRESUMPTIVE PROCEPHALIC LOBE.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS.  
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 CC -----  
 DR EMBL; M17120; AAA28312.1; -  
 DR EMBL; AL023873; CAA19641.1; -  
 DR EMBL; AE003417; AAF45498.1; -  
 DR PIR; A43731; A43731.  
 DR TRANSEAC; T00005; -  
 DR FlyBase; FBgn0000022; ac.  
 DR InterPro; IPR001092; HLH\_basic.  
 DR Pfam; PF00010; HLH; 1.  
 DR SMART; SM00353; HLH; 1.  
 DR PROSITE; PS00038; HLH\_1; 1.  
 DR PROSITE; PS00888; HLH\_2; 1.  
 KW Neurogenesis; Differentiation; Developmental protein; DNA-binding.  
 FT DNA\_BIND 27 37  
 FT DOMAIN 38 91  
 FT SEQUENCE 201 AA; 22753 MW; AAA906600CA764C0 CRC64;  
 SQ  
 Query Match 2.0%; Score 9; DB 1; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 399 QQQQQHQL 407  
 Db 115 QQQQQHQL 123  
 RESULT 13  
 ID P53\_EQUAS STANDARD; PRT; 207 AA.  
 AC Q29480;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53) (Fragment).  
 DE TP53.  
 OS Equus asinus (Donkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_Taxid:9793;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96342529; PubMed=8746464;  
 RA Nasir L., Reid S.W.;  
 RT "Nucleotide sequence of exons 5 to 9 of the p53 tumour-suppressor  
 RL gene of the donkey (*Equus asinus*).";  
 RL DNA Seq. 6:61-63(1995).  
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression (By similarity).  
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC -----  
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DR EMBL; U26741; AAB41265.1; -.  
 DR HSSP; P04637; 1TUP.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT NON\_TER 1  
 FT DNA\_BIND <1 168  
 FT DOMAIN 201 >207 BY SIMILARITY.  
 FT DOMAIN 187 199 OLIGOMERIZATION.  
 FT NON\_TER 207 207 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 SQ SEQUENCE 207 AA; 23428 MW; 973EBD85910B498E CRC64;  
 Query Match 2.0%; Score 9; DB 1; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 265 YNFMNCSSC 273  
 |||||  
 Db 110 YNFMNCSSC 118  
 RESULT 14  
 P53\_HORSE  
 ID P53\_HORSE STANDARD; PRT; 280 AA.  
 AC P79892; Q29481;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53) (Fragment).  
 GN TP53 OR P53.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE OF 1-263 FROM N.A.  
 RC TISSUE-Spleen;  
 RX MEDLINE=97070350; PubMed=8913276;  
 RA Pazzi K.A., Kraegel S.A., Griffey S.M., Theon A.P., Madewell B.R.;  
 RT "Analysis of the equine tumor suppressor gene p53 in the normal horse  
 and in eight cutaneous squamous cell carcinomas.";  
 RL Cancer Lett. 107:125-130(1996).  
 RN [2]  
 RP SEQUENCE OF 76-280 FROM N.A.  
 RX MEDLINE=96293865; PubMed=8722575;  
 RA Nasir L., Reid S.W.;  
 RT "Nucleotide sequence of exons 5 to 9 of the p53 tumour-suppressor  
 gene of the horse (Equus caballus).";  
 RL DNA Seq. 6:185-187(1996).  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 growth arrest or apoptosis depending on the physiological  
 circumstances and cell type. Involved in cell cycle regulation as  
 a trans-activator that acts to negatively regulate cell division  
 by controlling a set of genes required for this process. One of  
 the activated genes is an inhibitor of cyclin-dependent kinases.  
 Apoptosis induction seems to be mediated either by stimulation of  
 BAX and FAS antigen expression, or by repression of Bcl-2  
 expression (By similarity).  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 IN MANY TYPES OF CANCER.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
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 CC -----  
 DR EMBL; S83123; AAB46899.1; -.  
 DR EMBL; U37120; AAB18936.1; -.  
 DR HSSP; P04637; 1TUP.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT NON\_TER 1  
 FT DNA\_BIND 52 243 BY SIMILARITY.  
 FT DOMAIN 276 >280 OLIGOMERIZATION.  
 FT DOMAIN 262 274 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT CONFLICT 79 79 T -> A (IN REF. 2).  
 FT CONFLICT 83 83 L -> M (IN REF. 2).  
 FT CONFLICT 111 111 A -> V (IN REF. 2).  
 FT CONFLICT 138 138 G -> A (IN REF. 2).  
 FT NON\_TER 280 280  
 SQ SEQUENCE 280 AA; 30985 MW; 040F12030B5ACEE9 CRC64;  
 Query Match 2.0%; Score 9; DB 1; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 0.32;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 265 YNFMNCSSC 273  
 |||||  
 Db 185 YNFMNCSSC 193  
 RESULT 15  
 P53\_SPEBE  
 ID P53\_SPEBE STANDARD; PRT; 314 AA.  
 AC Q64662;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53) (Fragment).  
 GN TP53.  
 OS Spromophilus bechevii (Beechey ground squirrel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Spromophilus.  
 OX NCBI\_TaxID=34862;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Thymus;  
 RX MEDLINE=95007566; PubMed=7923176;  
 RA Rivkina M.B., Cullen J.M., Robinson W.S., Marlon P.L.;  
 RT "State of the p53 gene in hepatocellular carcinomas of ground  
 squirrels and woodchucks with past and ongoing infection with  
 hepatitisviruses.";  
 RL Cancer Res. 54:5430-5437(1994).  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 growth arrest or apoptosis depending on the physiological  
 circumstances and cell type. Involved in cell cycle regulation as  
 a trans-activator that acts to negatively regulate cell division  
 by controlling a set of genes required for this process. One of  
 the activated genes is an inhibitor of cyclin-dependent kinases.  
 Apoptosis induction seems to be mediated either by stimulation of  
 BAX and FAS antigen expression, or by repression of Bcl-2  
 expression.  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 IN MANY TYPES OF CANCER.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
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CC -----

DR EMBL; U43902; AA85628.1; -  
DR HSP; P04637; LYCS.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR ProDom; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Anti-Oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT NON\_TER 1  
FT DOMAIN 1 24  
FT DNA\_BIND 80 270  
FT DOMAIN 303 >314  
FT DOMAIN 289 301  
FT NON\_TER 314 314  
SQ SEQUENCE 314 AA; 34618 MW; 4F949656A8BED1F6 CRC64;

Query Match  
Best Local Similarity 2.0%; Score 9; DB 1; Length 314;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 275 GGMNRRPIL 283  
Db 222 GGMNRRPIL 230  
|||||||

Search completed: June 24, 2003, 22:26:09  
Job time : 16 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:25:12 ; Search time 19 Seconds  
(without alignments)  
2266.748 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 448

Sequence: 1 MSQSTQNEFLSPVFOHIW.....PKQSDVFRHKKPNRSVYP 448

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_73:\*  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	2.9	367	1 S02193	cellular tumor ant
2	13	2.9	396	1 JH0631	cellular tumor ant
3	10	2.2	393	2 JC6176	tumor suppressor p
4	10	2.2	396	1 JH0633	cellular tumor ant
5	9	2.0	201	2 A43731	Achaete-scute comp
6	9	2.0	363	1 A29376	cellular tumor ant
7	9	2.0	381	2 S38824	cellular tumor ant
8	9	2.0	386	1 S51648	cellular tumor ant
9	9	2.0	390	1 DNWS53	cellular tumor ant
10	9	2.0	391	1 S02192	cellular tumor ant
11	9	2.0	393	2 JC6193	tumor suppressor p
12	9	2.0	391	1 DNH053	cellular tumor ant
13	9	2.0	393	1 S06594	cellular tumor ant
14	9	2.0	481	2 A56346	transcription fact
15	9	2.0	629	2 A30168	homeotic protein L
16	9	2.0	635	2 S01164	homeotic protein L
17	9	2.0	678	1 A30350	dorsal protein - f
18	9	2.0	816	2 S46268	ataxin-1 - human
19	9	2.0	1062	2 G86325	hypothetical prote
20	9	2.0	1094	2 S49313	protein kinase - s
21	9	2.0	1145	2 T18235	transcription acti
22	9	2.0	1154	2 S9206	regulator protein
23	9	2.0	1394	2 B34598	ecdysone-induced p
24	9	2.0	1893	2 A56158	eye development pr
25	8	1.8	54	2 JU0155	spore protein gamm
26	8	1.8	77	2 I46226	cellular tumor ant
27	8	1.8	107	2 T25670	hypothetical prote
28	8	1.8	150	1 OKBYS1	cell division cont
29	8	1.8	158	2 F84776	probable RAV2-like

30	8	1.8	170	2 I50482	vimentin A1 - gold
31	8	1.8	173	2 A47303	FT2-F1 steroid rec
32	8	1.8	191	2 S35570	sex-determining pr
33	8	1.8	201	2 S23324	gene achaete prote
34	8	1.8	215	1 S61138	hypothetical prote
35	8	1.8	224	2 D46177	enhancer of split
36	8	1.8	230	2 T49555	related to high cy
37	8	1.8	243	2 T24981	hypothetical prote
38	8	1.8	255	2 A60637	merozoite antigen
39	8	1.8	264	1 WMTMCV	30K protein - cucu
40	8	1.8	264	1 WMTMSH	29K protein - cucu
41	8	1.8	265	2 A48121	retrovirus-related
42	8	1.8	267	1 S30863	BMH1 protein - yea
43	8	1.8	301	2 JW0079	heterogeneous nucl
44	8	1.8	330	2 A35915	homeotic protein A
45	8	1.8	390	1 B49070	ecdysone-inducible

ALIGNMENTS

RESULT 1

S02193  
cellular tumor antigen p53 - chicken  
N:Alternate names: nuclear oncoprotein p53  
C:Species: Gallus gallus (chicken)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S02193  
R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.  
Nucleic Acids Res. 16, 11383, 1988  
A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.  
A:Reference number: S02193; MUID:89083584; PMID:3060861  
A:Accession: S02193  
A:Molecule type: mRNA  
A:Residues: 1-367 <SD>  
A:Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:g63741  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho  
F:161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.9%; Score 13; DB 1; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	261	TTVLYNFMNCSSC	273
Db	216	TTVLYNFMNCSSC	228

RESULT 2

JH0631  
cellular tumor antigen p53 - rainbow trout  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JH0631  
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.  
Gene 112, 241-245, 1992  
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.  
A:Reference number: JH0631; MUID:92210006; PMID:1339362  
A:Accession: JH0631  
A:Molecule type: mRNA  
A:Residues: 1-396 <DEF>  
A:Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829  
A:Experimental source: liver  
C:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactiv  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho  
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.9%; Score 13; DB 1; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6.4e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 TTVLYNFCNMSC 273  
|||||  
Db 219 TTVLYNFCNMSC 231

## RESULT 3

JC6176

tumor suppressor protein p53 - Chinese hamster  
C:Species: Cricetulus griseus (Chinese hamster)

C:Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 23-Jul-1999

C:Accession: JC6176

R:Lee, H.; Larner, J.M.; Hamlin, J.L.

Gene 184, 177-183, 1997

A:Title: Cloning and characterization of Chinese hamster p53 cDNA.

A:Reference number: JC6176; MUID:97183659; PMID:9031625

A:Contents: liver

A:Accession: JC6176

A:Molecule type: mRNA

A:Residues: 1-393 &lt;LEE&gt;

A:Cross-references: GB:U50395; NID:g1842229; PIDN:AA53040.1; PID:g1842230

C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage  
ption, and recombination by protein/protein interactions.

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: liver; tumor

## Query Match

Best Local Similarity 2.2%; Score 10; DB 2; Length 393;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 RICACPGDR 313

|||||

Db 273 RICACPGDR 282

## RESULT 4

JH0633

cellular tumor antigen p53 - golden hamster  
N:Alternate names: tumor-suppressor protein p53

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: JH0633

R:Legros, Y.; McIntyre, P.; Soussi, T.

Gene 112, 247-250, 1992

A:Title: The cDNA cloning and immunological characterization of hamster p53.

A:Reference number: JH0633; MUID:92210007; PMID:1555773

A:Accession: JH0633

A:Molecule type: mRNA

A:Residues: 1-396 &lt;LEG&gt;

A:Cross-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415

A:Experimental source: Kidney, strain MP1

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph

F:179,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

C:Species: Drosophila melanogaster  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 21-Jul-2000  
C:Accession: A43731  
R:Villares, R.; Cabrera, C.V.  
Cell 50, 415-424, 1987

A:Title: The achaete-scute gene complex of Drosophila melanogaster: conserved domains

A:Reference number: A43731; MUID:87273503; PMID:3111716

A:Accession: A43731

A:Molecule type: DNA

A:Residues: 1-201 &lt;VIL&gt;

A:Cross-references: GB:M17120; NID:g156744; PIDN:AAA28312.1; PID:g156747

C:Genetics:

A:Gene: FlyBase:ac

A:Cross-references: FlyBase:FBgn0000022

C:Keywords: DNA binding

## Query Match

Best Local Similarity 2.0%; Score 9; DB 2; Length 201;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 QOQQQHQL 407

|||||

Db 115 QOQQQHQL 123

## RESULT 6

A29376

cellular tumor antigen p53 - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A29376; S61531; S72313; I51639

R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.

Oncogene 1, 71-78, 1987

A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a prot

A:Reference number: A29376; MUID:88143684; PMID:2830576

A:Accession: A29376

A:Molecule type: mRNA

A:Residues: 1-363 &lt;SOU&gt;

A:Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962

R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.

Oncogene 9, 109-120, 1994

A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopu

A:Reference number: I51639; MUID:94134403; PMID:8302570

A:Accession: S61531

A:Molecule type: mRNA

A:Residues: 1-293,295-363 &lt;HOE&gt;

A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.

submitted to the EMBL data Library, March 1994

A:Reference number: S72313

A:Accession: S72313

A:Molecule type: mRNA

A:Residues: 1-51,'S',53-70,72-293,295-363 &lt;HOE&gt;

A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F:150,153,213,217/Binding site: zinc (Cys, His, Cys) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

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F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

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F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

## Query Match

Best Local Similarity 2.0%; Score 9; DB 1; Length 363;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283

|||||

Db 219 GGMNRRPIL 227

## RESULT 7

S38824

Achaete-scute complex protein T5 - fruit fly (Drosophila melanogaster)

cellular tumor antigen p53, minor splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S3824; S35478  
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
Mol. Cell. Biol. 6, 3232-3239, 1986  
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.  
A:Reference number: S38822; MUID:87064640; PMID:3023970  
A:Accession: S38824  
A:Molecule type: mRNA  
A:Residues: 1-381 <ARA>  
A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203  
R:Han, K.A.; Kulesz-Martin, M.F.  
Nucleic Acids Res. 20, 1979-1981, 1992  
A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tissues.  
A:Reference number: S35478; MUID:92253421; PMID:1579500  
A:Accession: S35478  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-381 <HNA>  
A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988  
C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks the 5' not known.  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: alternative splicing; phosphoprotein; zinc  
F:1-44/Domain: transcription activation #status predicted <TRA>  
F:16-26/Region: conserved region I  
F:99-289/Domain: DNA-binding core #status predicted <DBC>  
F:108-121/Region: L1 loop  
F:114-139/Region: conserved region II  
F:160-192/Region: L2 loop  
F:168-178/Region: conserved region III  
F:231-252/Region: conserved region IV  
F:233-248/Region: L3 loop  
F:267-283/Region: conserved region V  
F:313-319/Region: nuclear location signal  
F:319-357/Region: tetramer association  
F:7-9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted  
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted  
Query Match 2.0%; Score 9; DB 2; Length 381;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283  
|||||||  
DB 241 GGMNRRPIL 249

RESULT 8  
S51648  
cellular tumor antigen p53 - bovine  
N:Alternate names: tumor-suppressor protein p53  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S51648  
R:Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.  
Submitted to the EMBL Data Library, September 1994  
A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its genomic organization.  
A:Reference number: S51648  
A:Accession: S51648  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-386 <DEQ>  
A:Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein; F:168-171-231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted  
Query Match 2.0%; Score 9; DB 1; Length 386;

Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 YNFMN SSC 273  
|||||||  
DB 227 YNFMN SSC 235

RESULT 9  
DNMS53  
cellular tumor antigen p53 - mouse  
N:Alternate names: oncoprotein p53  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Aug-1985 #sequence\_revision 04-Oct-1996 #text\_change 11-May-2000  
C:Accession: A22739; A02684; S38822; S38823; S40014; I48703  
R:Blenz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.  
EMBO J. 3, 2179-2183, 1984  
A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.  
A:Reference number: A22739; MUID:85027173; PMID:6092064  
A:Accession: A22739  
A:Molecule type: DNA  
A:Residues: 1-134, 'V', 136-390 <BIE>  
A:Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;  
R:Chumakov, P.M.  
Bioorg. Khim. 13, 1691-1694, 1987  
A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.  
A:Reference number: S06336; MUID:98221682; PMID:3329909  
A:Accession: S06336  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-134, 'V', 136-390 <CHU>  
R:Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.  
Nature 306, 594-597, 1983  
A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.  
A:Reference number: A02684; MUID:84068204; PMID:6646235  
A:Accession: A02684  
A:Molecule type: mRNA  
A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390 <ZAK>  
A:Cross-references: GB:X01237; GB:K01700; NID:g53575  
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
Mol. Cell. Biol. 6, 3232-3239, 1986  
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.  
A:Reference number: S38822; MUID:87064640; PMID:3023970  
A:Accession: S38822  
A:Molecule type: mRNA  
A:Residues: 1-390 <ARA1>  
A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199  
A:Accession: S38823  
A:Molecule type: mRNA  
A:Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>  
A:Cross-references: EMBL:M13873  
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
Submitted to the EMBL Data Library, July 1988  
A:Reference number: S40014  
A:Accession: S40014  
A:Molecule type: mRNA  
A:Residues: 1-167, 'G', 169-390 <ARA3>  
A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201  
R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.  
Nucleic Acids Res. 12, 5609-5626, 1984  
A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding p53.  
A:Reference number: I48703; MUID:84272240; PMID:6379601  
A:Accession: I48703  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>  
A:Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571  
C:Comment: This DNA-binding protein plays an essential role in the regulation of cell cycle. The tetramer association region may exhibit a beta-turn, beta-sheet, beta-strand.  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein; F:1-44/Domain: transcription activation #status predicted <TRA>  
F:16-26/Region: conserved region I

F:99-289/Domain: DNA-binding core #status predicted <DBC>  
 F:108-121/Region: L1 loop  
 F:114-139/Region: conserved region II  
 F:160-192/Region: L2 loop  
 F:168-178/Region: conserved region III  
 F:231-252/Region: conserved region IV  
 F:233-248/Region: L3 loop  
 F:267-283/Region: conserved region V  
 F:313-319/Region: nuclear location signal  
 F:319-357/Region: tetramer association  
 F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted  
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted  
 F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.0% Score 9; DB 1; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 0.81;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283  
 Db 241 GGMNRRPIL 249  
 |||||

RESULT 10  
 S02192  
 Cellular tumor antigen p53 - rat  
 N:Alternate names: gene p53 protein; nuclear oncoprotein p53  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S02192; S41149  
 R:Sousi, T.; de Fromental, C.C.; Breugnot, C.; May, E.  
 Nucleic Acids Res. 16, 11384, 1988  
 A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.  
 A:Reference number: S02192; MUID:89083585; PMID:3060862  
 A:Accession: S02192  
 A:Molecule type: mRNA  
 A:Residues: 1-391 <S02>  
 A:Cross-references: EMBL:X13058; NID:956828; PIDN:CAA31457.1; PID:956829  
 R:Hulla, J.E.; Schneider, R.P.  
 Nucleic Acids Res. 21, 713-717, 1993  
 A:Title: Structure of the rat p53 tumor suppressor gene.  
 A:Reference number: S41149; MUID:93181268; PMID:8441680  
 A:Accession: S41149  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-173, 'W', 175-391 <HUL>  
 A:Cross-references: EMBL:L07909  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
 C:Genetics:  
 A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2  
 C:Superfamily: cellular tumor antigen p53  
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho  
 F:174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
 F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.0% Score 9; DB 1; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 0.81;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283  
 Db 242 GGMNRRPIL 250  
 |||||

RESULT 11  
 JC6193  
 tumor suppressor p53 - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
 C:Accession: JC6193  
 R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.  
 Gene 185, 169-173, 1997

A:Title: cDNA cloning and immunological characterization of rabbit p53.  
 A:Reference number: JC6193; MUID:97208869; PMID:9055811  
 A:Accession: JC6193  
 A:Molecule type: mRNA  
 A:Residues: 1-391 <LEA>  
 A:Cross-references: EMBL:X90592; NID:91532043; PIDN:CAA62216.1; PID:91532044  
 C:Genetics:  
 A:Gene: p53  
 C:Superfamily: cellular tumor antigen p53  
 C:Keywords: tumor

Query Match 2.0% Score 9; DB 2; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 0.81;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283  
 Db 241 GGMNRRPIL 249  
 |||||

RESULT 12  
 DNH053  
 cellular tumor antigen p53 [validated] - human  
 N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor  
 C:Species: Homo sapiens (man)  
 C>Date: 05-Oct-1988 #sequence\_revision 18-Nov-1994 #text\_change 15-Sep-2000  
 C:Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; B25397.  
 4905; I58354; I78850; I52681; S60153  
 R:Lamb, P.; Crawford, L.  
 Mol. Cell. Biol. 6, 1379-1385, 1986  
 A:Title: Characterization of the human p53 gene.  
 A:Reference number: A25224; MUID:87064416; PMID:2946935  
 A:Accession: A25224  
 A:Molecule type: DNA  
 A:Residues: 1-393 <LAM>  
 A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:9189460; PIDN:AAA59987.1;  
 R:Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.  
 Gene 70, 245-252, 1988  
 A:Title: A variation in the structure of the protein-coding region of the human p53 gene  
 A:Reference number: JT0436; MUID:89108008; PMID:2905688  
 A:Accession: A43073  
 A:Molecule type: DNA  
 A:Residues: 1-393 <BUC1>  
 A:Cross-references: EMBL:M22898; NID:9189474  
 A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro  
 A:Accession: JT0436  
 A:Molecule type: DNA  
 A:Residues: 1-71, 'P', 73-393 <BUC2>  
 A:Cross-references: EMBL:M22898; NID:9189474; PIDN:AAA59988.1; PID:9189476  
 R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.  
 submitted to the EMBL Data Library, August 1990  
 A:Reference number: S40773  
 A:Accession: S40773  
 A:Molecule type: DNA  
 A:Residues: 1-393 <CHD>  
 A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214  
 R:Wiatlanski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.  
 EMBO J. 3, 3257-3262, 1984  
 A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the  
 A:Reference number: S42669; MUID:85126934; PMID:6396087  
 A:Accession: S42669  
 A:Molecule type: mRNA  
 A:Residues: 101-393 <MK11>  
 A:Cross-references: EMBL:X01405; NID:935215; PIDN:CAA25652.1; PID:9642241  
 R:Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.  
 EMBO J. 4, 1251-1255, 1985  
 A:Title: Human p53 cellular  
 A:Reference number: A22837; MUID:85230577; PMID:4006916  
 A:Accession: A22837  
 A:Molecule type: mRNA  
 A:Residues: 1-71, 'P', 73-393 <ZAK>  
 A:Cross-references: EMBL:X02469; EMBL:M60950; NID:935209; PIDN:CAA26306.1; PID:935210

R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.  
Mol. Cell. Biol. 5, 1601-1610, 1985  
A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tu  
A:Reference number: A55060; MUID:85267676; PMID:3894933  
A:Accession: A55060  
A:Molecule type: mRNA  
A:Residues: 1-71,'P',73-272,'H',274-393 <HAR>  
A:Cross-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479  
A:Experimental source: clone pR4-2, cell line A431  
R;Harris, N.; Brill, E.; Shohat, O.; Frokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.  
Mol. Cell. Biol. 6, 4650-4656, 1986  
A:Title: Molecular basis for heterogeneity of the human p53 protein.  
A:Reference number: A93086; MUID:87089826; PMID:3025664  
A:Accession: A25397  
A:Molecule type: mRNA  
A:Residues: 1-78,'T',80-393 <HAR1>  
A:Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814  
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line  
A:Accession: B25397  
A:Molecule type: mRNA  
A:Residues: 1-71,'P',73-78,'T',80-393 <HAR2>  
A:Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816  
A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line  
R;Maciashewski, G.J.; Tuck, S.; Plm, D.; Lamb, P.; Schneider, J.; Crawford, L.V.  
Mol. Cell. Biol. 7, 961-963, 1987  
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.  
A:Reference number: S42452; MUID:87144273; PMID:3547088  
A:Accession: S42452  
A:Molecule type: mRNA; DNA  
A:Residues: 66-71,'P',73-79 <MK12>  
A:Experimental source: clone lambda C113  
A:Note: 72-Cys was also found, and appears to represent a polymorphism  
A:Accession: S42453  
A:Molecule type: mRNA; DNA  
A:Residues: 66-79 <MK13>  
A:Experimental source: clone J6K  
R;Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.  
EMBO J. 10, 2879-2887, 1991  
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.  
A:Reference number: 138082; MUID:92007731; PMID:1915267  
A:Accession: 138082  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-189,'L',189-393 <F02>  
A:Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433  
A:Note: deletion of a C nucleotide causes a frameshift at position 566  
A:Accession: 138083  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-192,'R',194-393 <F02>  
A:Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435  
A:Accession: 138084  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-393 <F03>  
A:Cross-references: EMBL:X60012; NID:g506436; PIDN:CAA42627.1; PID:g506437  
A:Accession: 138085  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-245,'T',247-393 <F04>  
A:Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506439  
A:Accession: 138086  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236,'I',238-393 <F05>  
A:Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441  
A:Accession: 138087  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-247,'Q',249-393 <F06>  
A:Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443  
A:Accession: 138088  
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-71,'P',73-237,'Y',239-393 <F07>  
A:Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445  
A:Accession: 138089  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-247,'Q',249-393 <F08>  
A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447  
A:Accession: 138090  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-71,'P',73-162,'H',164-393 <F09>  
A:Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449  
A:Accession: 138091  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-212,'Q',214-393 <F10>  
A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451  
A:Accession: 138092  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-253,'D',255-393 <F11>  
A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453  
A:Note: all sequences submitted to the EMBL/Genbank/DBJ databases June 1991  
R;Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.  
Nucleic Acids Res. 19, 6977, 1991  
A:Title: An Alu polymorphism intragenic to the tp53 gene.  
A:Reference number: 138093; MUID:92107726; PMID:1762941  
A:Accession: 138093  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-393 <FUT>  
R;Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakata  
Cancer Res. 51, 5800-5805, 1991  
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell  
A:Reference number: A44905; MUID:92034678; PMID:1933850  
A:Accession: A44905  
A:Molecule type: DNA  
A:Residues: 246-247,'W',249-250 <YAM>  
A:Cross-references: GB:S63157; NID:g237829; PIDN:AAB20140.1; PID:g237830  
A:Note: sequence extracted from NCI backbone (NCBI:63157, NCBIP:63158)  
R;Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.  
Oncogene 6, 1067-1071, 1991  
A:Title: Use of the single strand conformation polymorphism technique and PCR to dete  
A:Reference number: 158354; MUID:91296386; PMID:1648702  
A:Accession: 158354  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 244-247,'W',249-252 <HEN1>  
A:Cross-references: GB:S41969; NID:g1679931; PIDN:AAB19324.1; PID:g232814  
A:Accession: 178850  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 274-277,'S',279-282 <HEN2>  
A:Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1; PID:g232816  
R;Chow, V.T.; Quek, H.H.; Tock, E.P.C.  
Cancer Lett. 73, 141-148, 1993  
A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lympho  
A:Reference number: 152681; MUID:94036762; PMID:8221626  
A:Accession: 152681  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 327-331,'DQTSFQKENC' <CHO>  
A:Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293  
A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-1  
R;Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.  
Mol. Gen. Genet. 249, 425-431, 1995  
A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fra  
A:Reference number: S60151; MUID:96133682; PMID:8552047  
A:Accession: S60153  
A:Molecule type: DNA

A:Residues: 3-44 <PET>  
R: Dang, C.V.; Lee, W.M.F.  
J. Biol. Chem. 264, 18019-18023, 1989  
A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70,

Query Match 2.0%; Score 9; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283  
|||||||  
Db 244 GGMNRRPIL 252

## RESULT 13

S06594

cellular tumor antigen p53 - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S06594

R: Rigaudy, P.; Eckhart, W.

Nucleic Acids Res. 17, 8375, 1989

A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p53.

A:Reference number: S06594; MUID:90045967; PMID:2530498

A:Accession: S06594

A:Molecule type: mRNA

A:Residues: 1-393 &lt;RIG&gt;

A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph

F:176,179,236,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 2.0%; Score 9; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GGMNRRPIL 283  
|||||||  
Db 244 GGMNRRPIL 252

## RESULT 14

A56346

transcription factor knl - fruit fly (Drosophila virilis)

C:Species: Drosophila virilis

C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 03-Dec-1999

C:Accession: A56346

R: Gerwin, N.; La Rosee, A.; Sauer, F.; Halbritter, H.P.; Neumann, M.; Jaekle, H.; Naube

Mol. Cell. Biol. 14, 7899-7908, 1994

A:Title: Functional and conserved domains of the Drosophila transcription factor encoded

A:Reference number: A56346; MUID:95059019; PMID:7969130

A:Accession: A56346

A&gt;Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-481 &lt;GER&gt;

A:Cross-references: GB:L36177; NID:g537507; PID:g537508

A:Note: authors translated the codon GCG for residue 403 as Pro

C:Genetics:

A:Gene: knirps

A:Cross-references: FlyBase:FBgn0013118

A:Introns: 26/3

Query Match 2.0%; Score 9; DB 2; Length 481;  
Best Local Similarity 100.0%; Pred. No. 0.97;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 QQQQQQHQL 406  
|||||||  
Db 135 QQQQQQHQL 143

## RESULT 15

A30168  
homeotic protein Labial - fruit fly (Drosophila sp.)  
C:Species: Drosophila sp.  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 17-Nov-2000

C:Accession: A30168; A24149

R: Diederich, R.J.; Merrill, V.K.L.; Pultz, M.A.; Kaufman, T.C.

Genes Dev. 3, 399-414, 1989

A:Title: Isolation, structure, and expression of Labial, a homeotic gene of the anten

A:Reference number: A30168; MUID:89252817; PMID:2566560

A:Accession: A30168

A:Molecule type: mRNA; DNA

A:Residues: 1-629 &lt;DIE&gt;

R: Hoey, T.; Doyle, H.J.; Harding, K.; Wedeen, C.; Levine, M.

Proc. Natl. Acad. Sci. U.S.A. 83, 4809-4813, 1986

A:Title: Homeo box gene expression in anterior and posterior regions of the Drosophil

A:Reference number: A24149; MUID:86259687; PMID:3014511

A:Accession: A24149

A:Molecule type: DNA

A:Residues: 501-561 &lt;HOE&gt;

C:Genetics:

A:Gene: FlyBase:lab

A:Cross-references: FlyBase:FBgn0002522

A:Introns: 406/1; 544/3

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:502-558/Domain: homeobox homology &lt;HOX&gt;

Query Match 2.0%; Score 9; DB 2; Length 629;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 QQQQQQHQL 407  
|||||||  
Db 51 QQQQQQHQL 59

Search completed: June 24, 2003, 22:29:48  
Job time : 20 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 24, 2003, 22:24:26 ; Search time 16 seconds  
(without alignments)  
823.842 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 448

Sequence: 1 MSQSTQTNELSPVFOHIW.....PKQSDVFRHKKPNRSVYP 448

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCRU5\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	448	US-09-643-597-340	Sequence 340, App
2	410	91.5	516	US-09-643-597-344	Sequence 344, App
3	410	91.5	641	US-09-643-597-339	Sequence 339, App
4	410	91.5	680	US-09-643-597-342	Sequence 342, App
5	341	76.1	461	US-09-643-597-343	Sequence 343, App
6	272	60.7	586	US-09-643-597-338	Sequence 338, App
7	269	60.0	356	US-09-643-597-341	Sequence 341, App
8	191	42.6	586	US-09-643-597-152	Sequence 152, App
9	22	4.9	635	US-09-081-975-3	Sequence 3, Appli
10	9	2.0	71	US-09-146-054-9	Sequence 9, Appli
11	9	2.0	71	US-09-664-977A-9	Sequence 9, Appli
12	9	2.0	169	US-08-094-071-3	Sequence 3, Appli
13	9	2.0	169	PCT-US92-00878-3	Sequence 3, Appli
14	9	2.0	170	US-08-094-071-2	Sequence 2, Appli
15	9	2.0	170	US-08-094-071-5	Sequence 5, Appli
16	9	2.0	170	US-08-094-071-6	Sequence 6, Appli
17	9	2.0	170	US-08-094-071-7	Sequence 7, Appli
18	9	2.0	170	PCT-US92-00878-2	Sequence 2, Appli
19	9	2.0	170	PCT-US92-00878-5	Sequence 5, Appli
20	9	2.0	170	PCT-US92-00878-6	Sequence 6, Appli
21	9	2.0	170	PCT-US92-00878-7	Sequence 7, Appli
22	9	2.0	271	US-09-414-436-1	Sequence 1, Appli
23	9	2.0	319	US-08-983-035A-42	Sequence 42, Appl
24	9	2.0	335	US-08-983-035A-44	Sequence 44, Appl
25	9	2.0	353	US-08-983-035A-40	Sequence 40, Appl
26	9	2.0	363	US-08-697-221-17	Sequence 17, Appl
27	9	2.0	363	US-08-697-221-18	Sequence 18, Appl

28	9	2.0	363	2	US-08-697-221-21	Sequence 21, Appl
29	9	2.0	363	2	US-08-697-221-22	Sequence 22, Appl
30	9	2.0	363	2	US-08-697-221-23	Sequence 23, Appl
31	9	2.0	363	2	US-08-697-221-24	Sequence 24, Appl
32	9	2.0	363	4	US-08-983-035A-26	Sequence 26, Appl
33	9	2.0	374	4	US-08-983-035A-28	Sequence 28, Appl
34	9	2.0	381	4	US-09-257-580-2	Sequence 2, Appli
35	9	2.0	381	4	US-08-983-035A-36	Sequence 36, Appl
36	9	2.0	390	1	US-08-347-792-15	Sequence 15, Appl
37	9	2.0	390	1	US-08-431-357-15	Sequence 15, Appl
38	9	2.0	390	4	US-08-392-542-3	Sequence 3, Appli
39	9	2.0	390	4	US-08-894-327-3	Sequence 3, Appli
40	9	2.0	390	4	US-09-685-027-3	Sequence 3, Appli
41	9	2.0	390	5	PCT-US95-15353-15	Sequence 15, Appl
42	9	2.0	393	1	US-08-047-041A-25	Sequence 25, Appl
43	9	2.0	393	1	US-08-047-041A-26	Sequence 26, Appl
44	9	2.0	393	1	US-08-047-041A-27	Sequence 27, Appl
45	9	2.0	393	1	US-08-047-041A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-09-643-597-340  
; Sequence 340, Application US/09643597  
; Patent No. 6426072  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skelky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455041  
; CURRENT APPLICATION NUMBER: US/09/643,597  
; CURRENT FILING DATE: 2006-08-21  
; NUMBER OF SEQ ID NOS: 369  
; SUMMARY: FASTA SEQ for Windows Version 3.0  
; SEQ ID NO 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-643-597-340

Query Match	100.0%;	Score 448;	DB 4;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSQSTQTNELSPVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI	RMQ	60
Db	1	MSQSTQTNELSPVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI	RMQ	60
Qy	61	DSLDSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	120	
Db	61	DSLDSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	120	
Qy	121	SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMT	180	
Db	121	SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMT	180	
Qy	181	PGQAVIRAMPYKKAHETVVKRCPNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDP	240	
Db	181	PGQAVIRAMPYKKAHETVVKRCPNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDP	240	
Qy	241	ITGRQSVLPVPEPQVGTEFTTVLYNFCNNSCVGMNRRPILIIIVTLETRDGOVLGRRC	300	

7/2 seqs  
Not claimed  
priority date 8/1/2002

us-09-670-568b-1.oli.ra

Mon Jun 30 08:33:12 2003

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Db      241  ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
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Db      301  FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
QY      361  LYLPLVGRREYEMLLKIKESLELMOYLPOHTIETIRYQOQOQOHHLLQKLLSACFRNE 420
Db      361  LYLPLVGRREYEMLLKIKESLELMOYLPOHTIETIRYQOQOQOHHLLQKLLSACFRNE 420
QY      421  LVEPRRETQKSDVFFRHSKPPNRSVYP 448
Db      421  LVEPRRETQKSDVFFRHSKPPNRSVYP 448
QY      421  LVEPRRETQKSDVFFRHSKPPNRSVYP 448
Db      421  LVEPRRETQKSDVFFRHSKPPNRSVYP 448

RESULT 2
US-09-643-597-344
; Sequence 344, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-643-597-344

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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 410; Conservative

QY      1  MSQSTQTNFLSPVEFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db      61  DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY      61  DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db      61  DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
Db      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
QY      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
Db      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
QY      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
Db      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
QY      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
Db      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
QY      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
Db      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
QY      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
Db      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360

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QY      361  LYLPLVGRREYEMLLKIKESLELMOYLPOHTIETIRYQOQOQOHHLLQK 410
Db      361  LYLPLVGRREYEMLLKIKESLELMOYLPOHTIETIRYQOQOQOHHLLQK 410

RESULT 3
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-643-597-339

Query Match          91.5%; Score 410; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 410; Conservative

QY      1  MSQSTQTNFLSPVEFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db      1  MSQSTQTNFLSPVEFQHWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY      61  DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db      61  DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY      61  DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db      61  DSDLSDPMPQYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
Db      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
QY      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
Db      121 SPSPAIPSNIDYFOPHSDVDFVFOQSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTTP 180
QY      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db      181 PQGAVIRAMPYVYKKAHVTEVVKCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
Db      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
QY      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
Db      241 ITGRQSVLPVPEPPQVTEFTVLYNFMNCSSCGVMNRRLIIVTLETRDQVGLGRC 300
QY      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
Db      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
QY      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360
Db      301 FEARICACGRDRKADEDSIRKQVSDSTKNGDKTKRPFQNTHTGQIOMTSIKKRRSPDDE 360

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RESULT 4
US-09-643-597-342
; Sequence 342, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

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;; COUNTRY: USA  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows  
;; SOFTWARE: FastSeq for Windows Version 2.0b  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/081,975  
;; FILING DATE: 12-MAY-1998  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/046,207  
;; FILING DATE: 12-MAY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Eisenstein, Ronald I  
;; REGISTRATION NUMBER: 30,628  
;; REFERENCE/DOCKET NUMBER: 47400  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-345-6054  
;; TELEFAX: 617-345-1300  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 635 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-09-081-975-3

Query Match 4.9%; Score 22; DB 4; Length 635;  
Best Local Similarity 100.0%; Pred. No. 1.8e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 LYNFMCNSSCVGGMNRRPILII 285

Db 253 LYNFMCNSSCVGGMNRRPILII 274

## RESULT 10

US-09-146-054-9  
; Sequence 9, Application US/09146054  
; Patent No. 632970  
; GENERAL INFORMATION:  
; APPLICANT: Little, Daniel  
; APPLICANT: Higgins, G. Scott  
; APPLICANT: Koster, Hubert  
; APPLICANT: Lough, David  
; APPLICANT: SEQUENOM, INC.  
; TITLE OF INVENTION: Mass Spectrometric Detection of Polypeptides  
; CURRENT APPLICATION NUMBER: US/09/146,054  
; CURRENT FILING DATE: 1998-09-02  
; EARLIER APPLICATION NUMBER: 08/922,201  
; EARLIER FILING DATE: 1997-09-02  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 71  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: REPEAT  
; LOCATION: (14)..(38)  
; OTHER INFORMATION: "gln" repeat region associated with spinal  
; OTHER INFORMATION: cerebellar ataxia 1 (SCA-1)  
; FEATURE:  
; NAME/KEY: REPEAT  
; LOCATION: (66)..(71)  
; OTHER INFORMATION: His-6 "tag"  
US-09-146-054-9

Query Match 2.0%; Score 9; DB 4; Length 71;

Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 398 QQQQQQHGH 406  
Db 20 QQQQQQHGH 28

## RESULT 11

US-09-664-977A-9  
; Sequence 9, Application US/09664977A  
; Patent No. 6387628  
; GENERAL INFORMATION:  
; APPLICANT: Little, Daniel  
; APPLICANT: Higgins, G. Scott  
; APPLICANT: Koster, Hubert  
; APPLICANT: Lough, David  
; TITLE OF INVENTION: Mass Spectrometric Detection of Polypeptides  
; FILE REFERENCE: 2016C  
; CURRENT APPLICATION NUMBER: US/09/664,977A  
; CURRENT FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 09/146,054  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 08/922,201  
; PRIOR FILING DATE: 1997-09-02  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 71  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: REPEAT  
; LOCATION: (14)..(38)  
; OTHER INFORMATION: "gln" repeat region associated with spinal  
; OTHER INFORMATION: cerebellar ataxia 1 (SCA-1)  
; NAME/KEY: REPEAT  
; LOCATION: (66)..(71)  
; OTHER INFORMATION: His-6 "tag"  
US-09-664-977A-9

Query Match 2.0%; Score 9; DB 4; Length 71;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 398 QQQQQQHGH 406

Db 20 QQQQQQHGH 28

## RESULT 12

US-08-094-071-3  
; Sequence 3, Application US/08094071  
; Patent No. 6083709  
; GENERAL INFORMATION:  
; APPLICANT: Reynolds, Frederick H.  
; APPLICANT: Sorvillo, John M.  
; APPLICANT: Zehed, Ron J.  
; APPLICANT: Stephenson, John R.  
; TITLE OF INVENTION: Immunoassay for Detection of  
; TITLE OF INVENTION: mutant p53 polypeptide in  
; TITLE OF INVENTION: biological fluids  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible

Query Match 2.0%; Score 9; DB 3; Length 169;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels

275 GGMNRRPIL 283  
|||||  
127 GGMNRRPIL 135

DB

RESULT 13  
PCT-US92-00878-3  
; sequence 3, Application PC/TUS9200878  
; GENERAL INFORMATION:  
; APPLICANT: Reynolds, Frederick H.  
; APPLICANT: Sorvillo, John M.  
; APPLICANT: Zeheb, Ron J.  
; APPLICANT: Stephenson, John R.  
; TITLE OF INVENTION: Immunoassay for Detection of mutant p53  
; TITLE OF INVENTION: polypeptide in biological fluids  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/00878  
; FILING DATE: 19920131  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 719,172  
; FILING DATE: 21-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 649,566  
; FILING DATE: 01-FEB-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 298,776  
; FILING DATE: 17-JAN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 298,837  
; FILING DATE: 18-JAN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 885,627  
; FILING DATE: 23-JUL-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 767,862  
; FILING DATE: 21-AUG-1985  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU 61540/86  
; FILING DATE: 18-AUG-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CA 516,260  
; FILING DATE: 19-AUG-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: NZ 217,209  
; FILING DATE: 14-AUG-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 23384-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525

TELEX: 422523 coop ui  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 169 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
IMMEDIATE SOURCE:  
CLONE: activated p53 oncogene  
PUBLICATION INFORMATION:  
AUTHORS: Bartek, J.  
AUTHORS: Iggo, R.  
AUTHORS: Lane, D. P.  
TITLE: Genetic and immunochemical analysis of mutant p53 in human breast cancer cell lines  
JOURNAL: Oncogene  
VOLUME: 5  
PAGES: 893-899  
DATE: 1990  
PCT-US92-00878-3

Query Match 2.0%; Score 9; DB 5; Length 169;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 GGMNRRPIL 283  
Db 127 GGMNRRPIL 135  
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RESULT 14  
US-08-094-071-2  
Sequence 2, Application US/08094071  
Patent No. 6083709  
GENERAL INFORMATION:  
APPLICANT: Reynolds, Frederick H.  
APPLICANT: Sorvilio, John M.  
APPLICANT: Zehnb, Ron J.  
TITLE OF INVENTION: Immunoassay for Detection of  
TITLE OF INVENTION: mutant p53 polypeptide in  
TITLE OF INVENTION: biological fluids  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/094,071  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 719,172  
FILING DATE: 21-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 649,566  
FILING DATE: 01-FEB-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 298,776  
FILING DATE: 17-JAN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 298,837

FILING DATE: 18-JAN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 885,627  
FILING DATE: 23-JUL-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 767,862  
FILING DATE: 21-AUG-1985  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU 61540/86  
FILING DATE: 18-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CA 516,260  
FILING DATE: 19-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 86.111 527.7  
FILING DATE: 20-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 195121/86  
FILING DATE: 20-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NZ 217,209  
FILING DATE: 14-AUG-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 23384-B  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 coop ui  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: N  
ANTI-SENSE: N  
IMMEDIATE SOURCE:  
CLONE: activated p53 oncogene  
PUBLICATION INFORMATION:  
AUTHORS: Bartek, J.  
AUTHORS: Iggo, R.  
AUTHORS: Lane, D. P.  
TITLE: Genetic and immunochemical analysis of  
TITLE: mutant p53 in human breast cancer cell lines  
JOURNAL: Oncogene  
VOLUME: 5  
PAGES: 893-899  
DATE: 1990  
US-08-094-071-2

Query Match 2.0%; Score 9; DB 3; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 GGMNRRPIL 283  
Db 128 GGMNRRPIL 136  
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RESULT 15  
US-08-094-071-5  
Sequence 5, Application US/08094071  
Patent No. 6083709  
GENERAL INFORMATION:  
APPLICANT: Reynolds, Frederick H.  
APPLICANT: Sorvilio, John M.  
APPLICANT: Zehnb, Ron J.  
TITLE OF INVENTION: Immunoassay for Detection of  
TITLE OF INVENTION: mutant p53 polypeptide in

;; TITLE OF INVENTION: biological fluids  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Cooper and Dunham  
;; STREET: 30 Rockefeller Plaza  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10112  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.24  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/094,071  
;; FILING DATE:  
;;  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 719,172  
;; FILING DATE: 21-JUN-1991  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 649,566  
;; FILING DATE: 01-FEB-1991  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 298,776  
;; FILING DATE: 17-JAN-1989  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 298,837  
;; FILING DATE: 18-JAN-1989  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 885,627  
;; FILING DATE: 23-JUL-1986  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 767,862  
;; FILING DATE: 21-AUG-1985  
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: AU 61540/86  
;; FILING DATE: 18-AUG-1986  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: CA 516,260  
;; FILING DATE: 19-AUG-1986  
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 86.111 527.7  
;; FILING DATE: 20-AUG-1986  
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 195121/86  
;; FILING DATE: 20-AUG-1986  
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: NZ 217,209  
;; FILING DATE: 14-AUG-1986  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: White, John P.  
;; REGISTRATION NUMBER: 28,678  
;; REFERENCE/DOCKET NUMBER: 23384-B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 977-9550  
;; TELEFAX: (212) 664-0525  
;; TELEX: 422523 COOP U1  
;;  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 170 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: N  
;; ANTI-SENSE: N  
;; IMMEDIATE SOURCE:  
;; CLONE: activated p53 oncogene  
;; PUBLICATION INFORMATION:  
;; AUTHORS: Bartek, J.  
;; AUTHORS: 1990, R.

;; AUTHORS: Lane, D. P.  
;; TITLE: Genetic and immunochemical analysis of mutant p53 in  
;; human breast cancer cell lines  
;; JOURNAL: Oncogene  
;; VOLUME: 5  
;; PAGES: 893-899  
;; DATE: 1990  
;; US-08-094-071-5

Query Match 2.0%; Score 9; DB 3; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 275 GGMNRRPIL 283  
|||||||  
DB 128 GGMNRRPIL 136

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Job time : 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 07:35:33 ; Search time 7008 Seconds  
(without alignments)  
11694.278 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816

Sequence: 1 tctgtgatcaaacagct.....gcattgtgtttaaaagaaa 2816

Scoring table:

OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*\*

- 1: gb\_ba:\*\*
- 2: gb\_htg:\*\*
- 3: gb\_in:\*\*
- 4: gb\_om:\*\*
- 5: gb\_ov:\*\*
- 6: gb\_pat:\*\*
- 7: gb\_ph:\*\*
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- 13: gb\_un:\*\*
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- 15: em\_ba:\*\*
- 16: em\_fun:\*\*
- 17: em\_hum:\*\*
- 18: em\_in:\*\*
- 19: em\_mu:\*\*
- 20: em\_om:\*\*
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- 23: em\_pat:\*\*
- 24: em\_ph:\*\*
- 25: em\_pl:\*\*
- 26: em\_ro:\*\*
- 27: em\_sts:\*\*
- 28: em\_un:\*\*
- 29: em\_vl:\*\*
- 30: em\_htg\_hum:\*\*
- 31: em\_htg\_inv:\*\*
- 32: em\_htg\_other:\*\*
- 33: em\_htg\_mus:\*\*
- 34: em\_htg\_pln:\*\*
- 35: em\_htg\_rnd:\*\*
- 36: em\_htg\_mam:\*\*
- 37: em\_htg\_vrt:\*\*
- 38: em\_sy:\*\*
- 39: em\_htgo\_hum:\*\*
- 40: em\_htgo\_mus:\*\*
- 41: em\_htgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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3	2816	100.0	2816	9	AB016072	AB016072 Homo sapi
4	1440	51.1	1516	9	FL16756S15	FL16756S15 Homo sapi
5	1433	50.9	180055	9	AC063939	AC063939 Homo sapi
6	1376	48.9	2031	9	AF116771	AF116771 Homo sapi
7	1376	48.9	2270	6	AX365939	AX365939 Sequence
8	1376	48.9	2270	6	BD000749	BD000749 Chimera g
9	1376	48.9	2270	9	AB016073	AB016073 Homo sapi
10	1347	47.8	1347	9	AF075428	AF075428 Homo sapi
11	1275	45.3	4846	6	AX009538	AX009538 Sequence
12	1275	45.3	4849	6	AX365942	AX365942 Sequence
13	1275	45.3	4849	9	HSA16961	Y16961 Homo sapien
14	1232	43.8	1551	6	AX365944	AX365944 Sequence
15	1232	43.8	1551	9	AF075432	AF075432 Homo sapi
16	1232	43.8	1926	9	AF075430	AF075430 Homo sapi
17	1141	40.5	1182	9	AF075429	AF075429 Homo sapi
18	1026	36.4	1386	6	AX365943	AX365943 Sequence
19	1026	36.4	1386	9	AF075433	AF075433 Homo sapi
20	1026	36.4	1761	9	AF075431	AF075431 Homo sapi
21	1005	35.7	4756	9	AF091627	AF091627 Homo sapi
22	975	34.6	2082	6	AX365941	AX365941 Sequence
23	975	34.6	2082	9	AF061512	AF061512 Homo sapi
24	826	29.3	4655	6	AX365758	AX365758 Sequence
25	822	29.2	2820	6	AX365938	AX365938 Sequence
26	822	29.2	2820	9	AB010153	AB010153 Homo sapi
27	720	25.6	1506	9	AB042841	AB042841 Homo sapi
28	659	23.4	699	9	HSA315499	AJ315499 Homo sapi
29	370	13.1	970	9	HSP63G13	AF124540 Homo sapi
30	257	9.1	508	9	FL16756S04	AF116759 Homo sapi
31	256	9.1	1193	9	HSP63G04	AF124531 Homo sapi
32	256	9.1	131166	2	AC117486	AC117486 Homo sapi
33	189	6.7	520	9	FL16756S05	AF116760 Homo sapi
34	189	6.7	859	9	HSP63G05	AF124532 Homo sapi
35	137	4.9	559	9	FL16756S10	AF116765 Homo sapi
36	137	4.9	618	9	FL16756S08	AF116763 Homo sapi
37	137	4.9	1237	9	HSP63G08	AF124535 Homo sapi
38	137	4.9	2451	9	HSP63G07	AF124534 Homo sapi
39	133	4.7	542	9	FL16756S02	AF116757 Homo sapi
40	133	4.7	1647	9	HSP63G02	AF124529 Homo sapi
41	119	4.2	662	9	FL16756S06	AF116761 Homo sapi
42	119	4.2	865	9	HSP63G06	AF124533 Homo sapi
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RESULT 1	AX365940	2816 bp	DNA	linear	PAT 15-FEB-2002
LOCUS	Sequence 333 from Patent WO0200174.				
DEFINITION	AX365940				
ACCESSION	AX365940.1	GI:18697449			
VERSION					
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	Wang, T., Wang, A., Skelky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A.,				
	Mcneill, P.D., Fanger, N., Retter, M.W., Marnierakis, N., Fanger, G.R.,				
	Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.				

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Compositions and methods for the therapy and diagnosis of lung cancer

Patent: WO 0200174-A 333 03-JAN-2002;  
CORIXA CORPORATION (US)

FEATURES  
source  
Location/Qualifiers  
i. .2816  
/organism="Homo sapiens"  
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BASE COUNT  
ORIGIN  
781 a 658 c 619 g 758 t

Query Match  
Best Local Similarity 100.0%; Score 2816; DB 6; Length 2816;  
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QY

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DB

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DB

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RESULT 2  
BD000748  
LOCUS BD000748 2816 bp DNA linear PAT 31-JAN-2002  
DEFINITION Chimera gene and chimera protein of p53 family.  
ACCESSION BD000748  
VERSION BD000748.1 GI:18623861  
KEYWORDS JP 2000354488-A/1.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2816)  
Ikawa.Y., Ikawa.S. and Tatewaki.M.  
Chimera gene and chimera protein of p53 family  
Patent: JP 2000354488-A 1 26-DEC-2000;  
JOURNAL

YOJI IGAWA, OTSUKA PHARMACEUTICAL CO LTD  
OS Homo sapiens (human)  
PN JP 2000354488-A/1  
PD 26-DEC-2000  
PF 09-APR-1999 JP 1999139034  
PR YOJI IGAWA, SHUNTARO IKAWA, MASUO TATEWAKI  
PI C12N15/09, C07K14/82, C07K19/00, C12N15/00  
PC  
CC  
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FT CDS (145)..(1488)  
FT polyA\_signal (2786)..(2791).  
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Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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## RESULT 3

AB016072

LOCUS

DEFINITION

AB016072

ACCESSION

VERSION

KEYWORDS

AB016072

Homo sapiens mRNA for p51A, complete cds.

AB016072

AB016072.1 GI:3510327

p51A.

2816 bp

mRNA

linear

PRI 06-FEB-1999

SOURCE Homo sapiens skeletal muscle cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Osada, M., Ohta, M., Kawahara, C., Ishioka, C., Kanamaru, R., Katoh, I.,  
Ikawa, Y., Nimura, Y., Nakagawara, A., Oshinaka, M. and Ikawa, S.  
TITLE Cloning and functional analysis of human p51, which structurally  
and functionally resembles p53  
JOURNAL Nat. Med. 4 (7), 839-843 (1998)  
MEDLINE 98324755  
REFERENCE 2 (bases 1 to 2816)  
AUTHORS Ikawa, S. and Osada, M.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUL-1998) Shuntaro Ikawa, Institute of Development,  
Aging and Cancer, Department of Cell Biology; 4-1 Seiryō-machi,  
Sendai, Miyagi 980-8575, Japan (E-mail: sikawa@idac.tohoku.ac.jp,  
Tel: 81-22-717-8484, Fax: 81-22-717-8488)  
FEATURES  
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DEFINITION	Homo sapiens p51 gene, exon 15 and complete cds, alternatively spliced		
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VERSION	15 of 15		
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SEGMENT	Homo sapiens		
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
ORGANISM	Tani.M., Shimizu.K., Kawahara.C., Kohno.T., Ishimoto.O., Ikawa.S. and Yokota,J.		
REFERENCE	Mutation and expression of the p51 gene in human lung cancer		
AUTHORS	Neoplasia 1 (1), 71-79 (1999)		
JOURNAL	20388515		
MEDLINE	10935472		
PUBMED	2 (bases 1 to 1516)		
REFERENCE	Tani.M., Shimizu.K., Kohno.T., Ikawa.S. and Yokota,J.		
AUTHORS	Direct Submission		
TITLE	Submitted (28-DEC-1998) Biology Division, National Cancer Center		
JOURNAL	Research Institute, 1-1. Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan		
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QY	2037	AGTGTACTGTGGCAGCGAGGTGATCATTTACCAAAAGTAATCAACTTTTGTGGTGGAGA	2096	

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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
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	Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,				
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	Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,				
	Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,				
	Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,				
	Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,				

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.K., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisegh, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Neilson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokwenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I., Sodergren, E., Sonaliker, F., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K., Wu, Y., Wu, Y., F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and Gibbs, R.

Direct Submission  
 Unpublished  
 2 (bases 1 to 180055)  
 Worley, K.C.

Direct Submission  
 Submitted (22-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 180055)  
 Worley, K.C.

Direct Submission  
 Submitted (27-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 4 (bases 1 to 180055)  
 Worley, K.C.

Direct Submission  
 Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Feb 27, 2002 this sequence version replaced qi:17933791.  
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email [gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

#### ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons

flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2031)  
 AUTHORS Tani,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.  
 TITLE Mutations and expression of the p51 gene in human lung cancer  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2031)  
 AUTHORS Tani,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-DEC-1998) Biology Division, National Cancer Center Research Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan

## FEATURES

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## RESULT 7

AX365939

LOCUS

Sequence 332 from Patent WO200174.

DEFINITION

AX365939

VERSION

AX365939.1

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

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AUTHORS

Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A.,

PAT 15-FEB-2002



Moneill, P.D., Fanger, N., Retter, M.W., Warnerakis, M., Fanger, G.R.,  
Vedick, T.S., Carter, D., Watanabe, Y., and Peckham, D.W.  
Compositions and methods for the therapy and diagnosis of lung  
cancer  
Patent: WO 0200174-A 332 03-JAN-2002;  
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ACCESSION BD000749  
VERSION BD000749.1 GI:18623862  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2270)  
AUTHORS Ikawa, Y., Ikawa, S. and Tatewaki, M.  
TITLE Chimera gene and chimera protein of p53 family  
JOURNAL Patent: JP 2000354488-A 2 26-DEC-2000;  
YOUJI IGAWA, OTSUKA PHARMACEUTICAL CO LTD  
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PN JP 2000354488-A/2  
PD 26-DEC-2000  
PF 09-APR-1999 JP 1999139034  
PR  
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DEFINITION	Homo sapiens mRNA for p51B, complete cds.
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VERSION	AB016073.1 GI:3510329
KEYWORDS	p51B.
SOURCE	Homo sapiens skeletal muscle cDNA to mRNA.
ORGANISM	Homo sapiens
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AUTHORS	Osada,M., Ohba,M., Kawahara,C., Ishioka,C., Kanamaru,R., Katoh,I., Ikawa,Y., Nimura,Y., Nakagawara,A., Ohinata,M. and Ikawa,S.
TITLE	Cloning and functional analysis of human p51, which structurally and functionally resembles p53
JOURNAL	Nat. Med. 4 (7), 839-843 (1998)
MEDLINE	98324755
REFERENCE	2 (bases 1 to 2270)
AUTHORS	Ikawa,S. and Osada,M.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-1998) Shuntaro Ikawa, Institute of Development, Aging and Cancer, Department of Cell Biology; 4-1 Seiryomachi, Sendai, Miyagi 980-8575, Japan (E-mail:sikawa@idac.tohoku.ac.jp, Tel:81-22-717-8484, Fax:81-22-717-8488)
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Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCTGCTCCCTCCCAACACGACTAC 540
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DEFINITION AF075428
ACCESSION AF075428
VERSION AF075428.1 GI:3695077
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1347)
AUTHORS Yang,A., Kaghad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotsch,V.,
Andrews,N.C., Caput,D. and McKeon,F.
TITLE p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
MOL. CELL 2 (3), 305-316 (1998)
JOURNAL
MEDLINE 98448095
PUBMED 9774969
REFERENCE 2 (bases 1 to 1347)
AUTHORS Yang,A., Kaghad,M., Caput,D. and McKeon,F.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
Longwood Ave, Boston, MA 02115, USA
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BASE COUNT 374 a 381 c 317 g 275 t
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Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 325 GACTCGACCTGAGTGACCCCATGTGSCACACGTACAGCAACCTGGGGCTTCCTGAACAGC 384  
DB 181 GACTCGACCTGAGTGACCCCATGTGSCACACGTACAGCAACCTGGGGCTTCCTGAACAGC 240  
QY 385 ATGGACAGCAGATTTCAGAACGGCTCCTCGTCCACCATGCTCCCTATTAACACAGACCCAGCG 444  
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QY 445 CAGAACAGCTCAGGGGGCTCGCCCTAGGCAACAGCCAGCTCCACCTTCGATGCTCTC 504  
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DB 222 TATATCTTCAGTTCCAGCCCATTCAGTGAACCTTTGGATGAACCATCAGAGATGTC 281  
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QY 342 CCCCAGTGGCCACAGTACAGCAACCTGGGGCTCTCGAAGCATGACAGCAGATTC 401  
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QY 402 GRACGCTCCTCGTCCACCGTCCCTATTAACACAGACACCGCGCAACAGCGTCAAGC 461

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Qy	582	CACGCCAAGTCGGCCACCTTGGAGTATTCACCTGAACTCAAGAAACTCTACTGCCAAAT	641
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Qy	702	CCGGCCATGCCCTGTCTACAAAAGCTGAGCAGCTCACGGAGTGGTGAAGCGGTGCC	761
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Qy	762	CAACCATGAGCTGAGCGCTGAATTCACGAGGACAGATTGCCCTCTAGTCAATTGAT	821
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Db	1122	GGCAGTACAAGAAACGGTGATGTGTACGAAGCGCCGTTTCGTGAGAACACATGGTAT	1181
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Db	882	TGTGCTGGTACCTTATGAGCCACCCAGGTGGCACTGAATTCACGACAGTCTTTGTACAA	941
Qy	942	TTTCATGTGTAAACAGCAGTGTGTGGAGGATGAACCGCGTCCAATTTTAATCATTTGT	1001
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Qy	1002	TACTCTGGAACACAGAGTGGCAAGTCTCTGGGCGGAGCTGTCTTGAGGCGCGGATCTG	1061
Db	1002	TACTCTGGAACACAGAGTGGCAAGTCTCTGGGCGGAGCTGTCTTGAGGCGCGGATCTG	1061
Qy	1062	TGCTTGCCCGAGGAAGACAGGAGGCGGATGAAGATAGCATCAAGAAAGCAGCAAGTTTC	1121
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Db	1302	GTACTTCTCCAGCAGACATTTGAACGTACAGCAACGCAACGCAAGCAGCAGCAGCAGCA	1361
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1 (bases 1 to 1551)
Yang,A., Kaghad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotsch,V.,
Andrews,N.C., Caput,D. and McKeon,F.
p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
Mol. Cell 2 (3), 305-316 (1998)
JOURNAL
MEDLINE 98448095
PUBMED 9774969
REFERENCE 2 (bases 1 to 1551)
Yang,A., Kaghad,M., Caput,D. and McKeon,F.
Direct Submission
TITLE Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
Longwood Ave, Boston, MA 02115, USA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3q27-q29"
1..1551
/function="transcription factor"
/note="fifth splice variant; related to p53 and p73"
/codon_start=1
/product="TA p63 beta"
/protein_id="AAC62637.1"
/db_xref="GI:3695086"
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SVTAPSPYAPQSPSTFDALSPSPALNTDYPGPHSPDVSQSSSTAKSATWTYSTELK
KLYQIAKTCPIQIKVYTPPGAVIRAMPVYKAEHVTVEVVKRCPNHELSEFNEGO
IAPPSHLIIEVGNHQAQVEDPITGQSVLPVEPQVGTETVLYNPMCHNSCVGG
MNRRLPIIVTLETRGQVLGRRCFEARICAPGRDKADESIRKQVSDSTKNGDG
TKRPFQNTHTQMTSIRKRRSPDDELLYLPVRGTYEMLLKIKESLEIMQYLPQHT
IETRYQQQOQHLLQKQTSIQSPSSYGNSSPPLNKNMKNLPSVQLINPQQRNA
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SIVRIWQV"
BASE COUNT 425 a 466 c 350 g 310 t
ORIGIN

Query Match 43.8%; Score 1232; DB 9; Length 1551;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db
1 ATGTCAGAGCAGCAGACAAATGAATTCCTCAGTCAGAGAGTTTTCAGCATATCTGG 60
QY 205 GATTTCCTGGAACAGCCTATATGTTTCAGTTCAGCCCATTCAGTTCGATGATGAA 264
Db
61 GATTTCCTGGAACAGCCTATATGTTTCAGTTCAGCCCATTCAGTTCGATGATGAA 120
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Qy 1345 CAGCAGCAGCACCAGCAGCTTACTTCAGAAACA 1376  
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Db 1201 CAGCAGCAGCACCAGCAGCTTACTTCAGAAACA 1232  
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Job time : 7013 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 07:59:43 ; Search time 157 Seconds  
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5500.648 Million cell updates/sec

Title: US-09-670-568B-2

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1275	45.3	4849	4	US-09-643-597-335
4	1232	43.8	1551	4	US-09-643-597-337
5	1026	36.4	1386	4	US-09-643-597-336
6	975	34.6	2082	4	US-09-643-597-334
7	826	29.3	4655	4	US-09-643-597-151
8	822	29.2	2820	4	US-09-643-597-331
9	24	0.9	279	4	US-09-438-906-12
c 10	23	0.8	39	1	US-08-222-177A-86
c 11	23	0.8	40	1	US-08-222-177A-152
c 12	23	0.8	54	1	US-08-469-802B-27
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c 24	23	0.8	283	4	US-08-458-745-11
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c 27	23	0.8	564	1	US-08-117-362-32

ALIGNMENTS

RESULT 1

US-09-643-597-333  
: Sequence 333, Application US/09643597  
: Patent No. 6426072

: GENERAL INFORMATION:  
: APPLICANT: Wang, Tongtong

: APPLICANT: Fan, Liqun

: APPLICANT: Kalos, Michael D.

: APPLICANT: Bangur, Chaitanya S.

: APPLICANT: Hosken, Nancy

: APPLICANT: Fanger, Gary R.

: APPLICANT: Li, Samuel X.

: APPLICANT: Wang, Aijun

: APPLICANT: Skeiky, Yasir A.W.

: APPLICANT: Henderson, Robert A.

: APPLICANT: McNeill, Patricia D.

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

: FILE REFERENCE: 210121.455C11

: CURRENT APPLICATION NUMBER: US/09/643,597

: CURRENT FILING DATE: 2000-08-21

: NUMBER OF SEQ ID NOS: 369

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 333

: LENGTH: 2816

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-643-597-333

Query Match 100.0%; Score 2816; DB 4; Length 2816;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTTTGG	120
Db	61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAACCCAGCTCATTTCTTTGG	120
Qy	121	AAGAAAGTTATTACCGATCCACATGTCCTCAGAGCACACAGACAAATGAATTCCTCAGT	180
Db	121	AAGAAAGTTATTACCGATCCACATGTCCTCAGAGCACACAGACAAATGAATTCCTCAGT	180
Qy	181	CCAGAGTTTTCAGCATATCTGGGATTTTCTGGAAGCCCTATATCTTCAGTTCAGCCC	240
Db	181	CCAGAGTTTTCAGCATATCTGGGATTTTCTGGAAGCCCTATATCTTCAGTTCAGCCC	240
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Db	241	 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGGACAAAACAAGATTGAGATT	300
Qy	301	AGCATGGACTGTATCGGATCGAGACTCGGACCTGAGTGAACCCCATGTCGCCACAGTAC	360
Db	301	AGCATGGACTGTATCGGATCGAGACTCGGACCTGAGTGAACCCCATGTCGCCACAGTAC	360
Qy	361	ACGAACCTGGGGCTCTGAACAGCATGACAGACAGATTCAGAAGGCTCCTGTCGTCACC	420
Db	361	ACGAACCTGGGGCTCCTGAACAGCATGACAGACAGATTCAGAAGGCTCCTGTCGTCACC	420
Qy	421	AGTCCCTATTAAACACAGACCACGCGACAGACAGCGTACGGGCGCCTCGCCCTAGCCACAG	480
Db	421	AGTCCCTATTAAACACAGACCACGCGAGAACAGCGTACGGGCGCCTCGCCCTAGCCACAG	480
Qy	481	CCAGCTCCACCTTCGATGCTCTCTCCATCACCGGCCATCCCTCCAAACACCGACTAC	540
Db	481	CCAGCTCCACCTTCGATGCTCTCTCCATCACCGGCCATCCCTCCAAACACCGACTAC	540
Qy	541	CGAGGCCCGACAGTTTCGACGTGTCCTTCACGACAGTCGACACCGCCCAAGTCGGCCACC	600
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Db	601	TGACGATATTCGACTGAATGAAGAAACTCTACTGCCAAATGCAAAAGACATGCCCATC	660
Qy	661	CAGATCAAGGTGATGACCCCACTCCTCAGGAGCTGTTATCCGGCCATGCCCTGTCTAC	720
Db	661	CAGATCAAGGTGATGACCCCACTCCTCAGGAGCTGTTATCCGGCCATGCCCTGTCTAC	720
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Qy	781	GAATTCACAGGAGGACAGATTGCCCTCCTAGTCAATTTGATTCGAGTAGAGGGAACAGC	840
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Qy	841	CATGCCAGTATGTAGAAGATCCCATCAGAGACAGAGAGTGCCTGGTACCTTATGAG	900
Db	841	CATGCCAGTATGTAGAAGATCCCATCAGAGACAGAGAGTGCCTGGTACCTTATGAG	900
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Db	901	CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAAATTCATGTGTAACAGCAGT	960
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Db	1021	GGGCAAGTCTCGGGCGAGCTGCTTTGAGGCCCGGATCTGTGTTGCCACAGGAAGAGAC	1080
Qy	1081	AGGAAGCGGATGAAGATAGCATAGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGT	1140
Db	1081	AGGAAGCGGATGAAGATAGCATAGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGT	1140
Qy	1141	GATGGTACGAAGCGCGCTTCGTGACAGACACATGTTATCCAGATGACATCCATCAAG	1200
Db	1141	GATGGTACGAAGCGCGCTTCGTGACAGACACATGTTATCCAGATGACATCCATCAAG	1200
Qy	1201	AAACGAAGATCCCCAGATGATGAACCTGTTATCTTACCAGTGAAGGCCGTGAGACTTAT	1260
Db	1201	AAACGAAGATCCCCAGATGATGAACCTGTTATCTTACCAGTGAAGGCCGTGAGACTTAT	1260
Qy	1261	GAATGCTGTTGAAGATCAAGAGTCCCTGGAGCTCATGCACTACCTTCCTCAGCACACA	1320
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Qy	1321	ATTGAAACGTTACAGGCAACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1380





FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 337  
LENGTH: 1551  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-643-597-337

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 265 CCATCAGAAGATGTCGGCAACAAAGATTGAGATTAGCATTTGATGAGTATCCGATCAG 324  
DB 121 CCATCAGAAGATGTCGGCAACAAAGATTGAGATTAGCATTTGATGAGTATCCGATCAG 180  
QY 325 GACTCGACCTGAGTACCCCATGTCGCCAGTACACAGCAACCTGGGGCTCCTGAACAGC 384  
DB 181 GACTCGACCTGAGTACCCCATGTCGCCAGTACACAGCAACCTGGGGCTCCTGAACAGC 240  
QY 385 ATGGACGACGAGATTCAGAACGGCTCCTCGTCCACCACTGCTTATACACAGACACGCG 444  
DB 241 ATGGACGACGAGATTCAGAACGGCTCCTCGTCCACCACTGCTTATACACAGACACGCG 300  
QY 445 CAGAACAGCTCAGGGGGCCCTCGCCCTACGACAGCCCACTGCTTATACAGTGTCTC 504  
DB 301 CAGAACAGCTCAGGGGGCCCTCGCCCTACGACAGCCCACTGCTTATACAGTGTCTC 360  
QY 505 TCTCATCACCGGCATCCCTCCACACAGCTACCCAGCCGCGCAGTTTCGACGTG 564  
DB 361 TCTCATCACCGGCATCCCTCCACACAGCTACCCAGCCGCGCAGTTTCGACGTG 420  
QY 565 TCCTTCAGCAGTCGACGACCCGCAAGTCGCGCCACCTGGAGCTTATTCAGTGAAGTGAAG 624  
DB 421 TCCTTCAGCAGTCGACGACCCGCAAGTCGCGCCACCTGGAGCTTATTCAGTGAAGTGAAG 480  
QY 625 AAATCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684  
DB 481 AAATCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 540  
QY 685 CCTCAGGAGCTGTTATCCCGGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAG 744  
DB 541 CCTCAGGAGCTGTTATCCCGGCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGGAG 600  
QY 745 GTGGTGAAGGGTGCCTCCCAACCATGAGTGCAGCGTGAATTCACAGGAGGACAGATGCC 804  
DB 601 GTGGTGAAGGGTGCCTCCCAACCATGAGTGCAGCGTGAATTCACAGGAGGACAGATGCC 660  
QY 805 CCTCCTAGTCATTTGATTCAGTAGAGGGGAACAGCCATGCCCATGTATGTAGAGATCCC 864  
DB 661 CCTCCTAGTCATTTGATTCAGTAGAGGGGAACAGCCATGCCCATGTATGTAGAGATCCC 720  
QY 865 ATCAGAGAGACAGAGTGTCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 924  
DB 721 ATCAGAGAGACAGAGTGTCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 780  
QY 925 ACAGACCTCTGTACAAATTTTCATGTGAACAGAGTTGTGTGGAGGGATGAACCGCGT 984  
DB 781 ACAGACCTCTGTACAAATTTTCATGTGAACAGAGTTGTGTGGAGGGATGAACCGCGT 840  
QY 985 CCAATTTTAAATCTACTCTGGAAACACAGATGGGCAAGTCTCTGGGGCCGACGTGC 1044  
DB 1044 CCAATTTTAAATCTACTCTGGAAACACAGATGGGCAAGTCTCTGGGGCCGACGTGC

RESULT 5

US-09-643-597-336  
Sequence 336, Application US/09643597  
Patent No. 6426072  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 336  
LENGTH: 1386  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-643-597-336

Query Match 36.4%; Score 1026; DB 4; Length 1386;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1026; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 42 GCCACAGTACACGAACCTGGGGCTCCTGAACAGCATGGACCCAGAGATTCAGAACGGCTC 101  
QY 411 CTCGTCCACAGTCCCTTATACACAGACCCAGCCAGAACGCTCAGCGGCCCTCGCC 470  
DB 102 CTCGTCCACAGTCCCTTATACACAGACCCAGCCAGAACGCTCAGCGGCCCTCGCC 161  
QY 471 CTAGGCACACCCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTCCAA 530  
DB 162 CTAGGCACACCCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTCCAA 221  
QY 531 CACCGACTACCCAGGCCGCGACAGTTTCGAGGTGCTCTCCAGCAGTCGAGCAGCCGCAA 590

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222  CACCGACTACCGAGCCGCGCAGACATTTCCAGCTGTCTTCCAGCAGTCGAGCAGCGCAA 281
QY  591  GTGGCCACCTGGACGATTTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGAAGAC 650
Db  282  GTGGCCACCTGGACGATTTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGAAGAC 341
QY  651  ATGCCCCATCAGATCAAGTGATGACCCCACTCTCTCAGGGAGCTGTATTCGCGGCAT 710
Db  342  ATGCCCCATCAGATCAAGTGATGACCCCACTCTCTCAGGGAGCTGTATTCGCGGCAT 401
QY  711  GCCTGTCTACAAAAGCTGAGCAGCTGAGGAGGTGGTGAACGGTGCCCAACCATGA 770
Db  402  GCCTGTCTACAAAAGCTGAGCAGCTGAGGAGGTGGTGAACGGTGCCCAACCATGA 461
QY  771  GCTGAGCGGTGAATTCACAGGAGGAGATTTGCCCTCTCTAGTCAATTTGATTCAGTAGA 830
Db  462  GCTGAGCGGTGAATTCACAGGAGGAGATTTGCCCTCTCTAGTCAATTTGATTCAGTAGA 521
QY  831  GGGGACAGCGCATGCCAGTATGTAGAATCCCATCACAGGAAGACAGAGTGTCTGGT 890
Db  522  GGGGACAGCGCATGCCAGTATGTAGAATCCCATCACAGGAAGACAGAGTGTCTGGT 581
QY  891  ACCTTATGAGCCACCCAGCTTGGCACTGAATTCAGCAGAGTCTTGTACAAATTCATGTG 950
Db  582  ACCTTATGAGCCACCCAGCTTGGCACTGAATTCAGCAGAGTCTTGTACAAATTCATGTG 641
QY  951  TAACAGAGTGTGTGGAGGATGAACCGCGCTCCCAATTTAATCATTTGTTACTCTGGA 1010
Db  642  TAACAGAGTGTGTGGAGGATGAACCGCGCTCCCAATTTAATCATTTGTTACTCTGGA 701
QY  1011  AACCCAGATGGCAAGTCTGGGCGAGCTGCTTTGAGGCGCGGATCTGTGCTTGCCTCC 1070
Db  702  AACCCAGATGGCAAGTCTGGGCGAGCTGCTTTGAGGCGCGGATCTGTGCTTGCCTCC 761
QY  1071  AGGAAGACAGGAGGCGGATGAAGTAGCATCAGAAAGCAGCAAGTTTCGACAGTAC 1130
Db  762  AGGAAGACAGGAGGCGGATGAAGTAGCATCAGAAAGCAGCAAGTTTCGACAGTAC 821
QY  1131  AAGAAGCGTGATGTGACGAAGCGCGCTTTCGTCAAGACACACATGGTATCCAGATGAC 1190
Db  822  AAGAAGCGTGATGTGACGAAGCGCGCTTTCGTCAAGACACACATGGTATCCAGATGAC 881
QY  1191  ATCCATCAAGAAGCAAGATCCCGAGATGATGAACGTGTTATCTTACAGTGAAGGCGCG 1250
Db  882  ATCCATCAAGAAGCAAGATCCCGAGATGATGAACGTGTTATCTTACAGTGAAGGCGCG 941
QY  1251  TGAGACTTATGAATCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCACTTACCTCC 1310
Db  942  TGAGACTTATGAATCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCACTTACCTCC 1001
QY  1311  TCAGCACAAATTTGAACCTTACAGGCAAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGT 1370
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RESULT 6  
 US-09-643-597-334  
 ; Sequence 334, Application US/09643597  
 ; Patent No. 6426072  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Fan, Liqun  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Hosken, Nancy  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Li, Samuel X.  
 ; APPLICANT: Wang, Aijun

```

; APPLICANT: Skeiky, Yasir A.W.  

; APPLICANT: Henderson, Robert A.  

; APPLICANT: McNeill, Patricia D.  

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  

; FILE REFERENCE: 210121.455C11  

; CURRENT FILING DATE: 2000-08-21  

; NUMBER OF SEQ ID NOS: 369  

; SOFTWARE: FastSeq for Windows Version 3.0  

; SEQ ID NO 334  

; LENGTH: 2082  

; TYPE: DNA  

; ORGANISM: Homo sapiens  

US-09-643-597-334

Query Match 34.6%; Score 975; DB 4; Length 2082;  

Best Local Similarity 99.9%; Pred. No. 0;  

Matches 1025; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 351 GCCACAGTACAGAACTCGGGCTCTGAACAGCATGGACAGCATTCAGAACGGCTC 410
Db 477 GCCACAGTACAGAACTCGGGCTCTGAACAGCATGGACAGCATTCAGAACGGCTC 536
QY 411 CTGCTCCACAGTCCCTATTAACACAGCACGCGCAGAAAGCGTCCACGCGCCCTCGCC 470
Db 537 CTGCTCCACAGTCCCTATTAACACAGCACGCGCAGAAAGCGTCCACGCGCCCTCGCC 596
QY 471 CTACGACAGCCAGCTCCACCTTCAGTCTCTCTCTCCATACCGCGCATCCCTCCAA 530
Db 597 CTACGACAGCCAGCTCCACCTTCAGTCTCTCTCTCCATACCGCGCATCCCTCCAA 656
QY 531 CACCGACTACCGAGCCGCGCAGATTTCCAGCTGTCTCTTCCAGCAGTCGACAGCCGCA 590
Db 657 CACCGACTACCGAGCCGCGCAGATTTCCAGCTGTCTCTTCCAGCAGTCGACAGCCGCA 716
QY 591 GTCGGCCACTGGACGATTTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGAAAGAC 650
Db 717 GTCGGCCACTGGACGATTTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGAAAGAC 776
QY 651 ATGCCCATCCAGATCAAGTGTACCCCACTCTCTCAGGAGCTGTTATCCGCGCAT 710
Db 777 ATGCCCATCCAGATCAAGTGTACCCCACTCTCTCAGGAGCTGTTATCCGCGCAT 836
QY 711 GCCTGTCTACAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCAACCATGA 770
Db 837 GCCTGTCTACAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCAACCATGA 896
QY 771 GCTGAGCGGTGAATTCACAGGAGGAGATTTGCCCTCTCTAGTCAATTTGATTCGAGTAGA 830
Db 897 GCTGAGCGGTGAATTCACAGGAGGAGATTTGCCCTCTCTAGTCAATTTGATTCGAGTAGA 956
QY 831 GGGGAACGCCATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTCTGGT 890
Db 957 GGGGAACGCCATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTCTGGT 1016
QY 891 ACCTTATGAGCCACCCAGTGTGGCAGTGAATTCAGACAGCTTGTGTACAATTTTCATGTG 950
Db 1017 ACCTTATGAGCCACCCAGTGTGGCAGTGAATTCAGACAGCTTGTGTACAATTTTCATGTG 1076
QY 951 TAAACAGAGTGTGTGGAGGATGAACCGCGCTCTCTGAGGCGCGGATCTGTGCTTGTCTGGA 1010
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QY 1011 AACCCAGATGGCAAGTCTGGGCGAGCTGCTTTCAGGCGCGGATCTGTGCTTGTGCC 1070
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QY 1071 AGGAAGACAGGAGGCGGATGAAGTAGCATCAGAAAGCAGAAAGTTTCGACAGTAC 1130
Db 1197 AGGAAGACAGGAGGCGGATGAAGTAGCATCAGAAAGCAGAAAGTTTCGACAGTAC 1256
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IMMEDIATE SOURCE:  
CLONE: mfd12rs  
US-08-222-177A-86

Query Match 0.8%; Score 23; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1546 GTGTGTGTGTGTGTGTGTGTG 1568  
Db 36 GTGTGTGTGTGTGTGTGTGTG 14

## RESULT 11

US-08-222-177A-152/c  
Sequence 152, Application US/08222177A  
Patent No. 5582979  
GENERAL INFORMATION:  
APPLICANT: Weber, James L.  
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
TITLE OF INVENTION: (GC-GA)n.(GG-GT)n SEQUENCES AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 460  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dewitt Ross & Stevens, S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53717-1914

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/222,177A  
APPLICATION NUMBER: 08/222,177A  
FILING DATE: 21-APR-1989

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/341,562  
FILING DATE: 21-APR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 09865,601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 831-2100  
TELEFAX: (608) 831-2106  
TELEX:

INFORMATION FOR SEQ ID NO: 152:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
IMMEDIATE SOURCE:  
CLONE: mfd34rs  
US-08-222-177A-152

Query Match 0.8%; Score 23; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1546 GTGTGTGTGTGTGTGTGTGTG 1568  
Db 24 GTGTGTGTGTGTGTGTGTGTG 2

## RESULT 12

US-08-469-802B-27/c  
Sequence 27, Application US/08469802B  
Patent No. 5741645

GENERAL INFORMATION:  
APPLICANT: Orr, Harry T.  
APPLICANT: Ranum, Laura P.W.  
APPLICANT: Chung, Ming-yi  
APPLICANT: Zoghdi, Huda Y.  
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia  
Patent No. 5741645  
TITLE OF INVENTION: Type 1 and Method for Diagnosis  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muetling, Raasch, Gebhardt & Schwappach, P.A.  
STREET: 119 No. 5741645th Fourth Street, Suite 203  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/469,802B  
APPLICATION NUMBER: 08/469,802B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Muetling, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110.00030101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1225

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-469-802B-27

Query Match 0.8%; Score 23; DB 1; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1546 GTGTGTGTGTGTGTGTGTGTG 1568  
Db 47 GTGTGTGTGTGTGTGTGTGTG 25

## RESULT 13

US-08-267-803B-45/c  
Sequence 45, Application US/08267803B  
Patent No. 5834183  
GENERAL INFORMATION:  
APPLICANT: Orr, Harry T.  
APPLICANT: Ranum, Laura P.W.  
APPLICANT: Chung, Ming-yi  
APPLICANT: Zoghdi, Huda Y.  
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia  
Patent No. 5834183

TITLE OF INVENTION: Type 1 and Method for Diagnosis  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muetling, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/267,803B  
FILING DATE: 28-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McCormack, Myra H.  
REGISTRATION NUMBER: 36,602  
REFERENCE/DOCKET NUMBER: 110.00030120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-267-803B-45

Query Match 0.8%; Score 23; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTGTG 1568  
|||||  
DB 47 GTGTGTGTGTGTGTGTGTGTGTG 25

RESULT 14  
US-08-222-177A-149/c  
Sequence 149, Application US/08222177A  
Patent No. 5582979  
GENERAL INFORMATION:  
APPLICANT: Weber, James L.  
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
(dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 460  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dewitt Ross & Stevens, S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53717-1914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,177A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/341,562  
FILING DATE: 21-APR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 09865.601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 831-2100  
TELEFAX: (608) 831-2106  
TELEX:  
INFORMATION FOR SEQ ID NO: 149:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 56 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
IMMEDIATE SOURCE:  
CLONE: mfd33rs  
US-08-222-177A-149

Query Match 0.8%; Score 23; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTGTG 1568  
|||||  
DB 44 GTGTGTGTGTGTGTGTGTGTGTG 22

RESULT 15  
US-08-469-802B-29  
Sequence 29, Application US/08469802B  
Patent No. 5741645  
GENERAL INFORMATION:  
APPLICANT: Orr, Harry T.  
APPLICANT: Rannum, Laura P.W.  
APPLICANT: Chung, Ming-yi  
APPLICANT: Zoghbi, Huda Y.  
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia  
Patent No. 5741645  
TITLE OF INVENTION: Type 1 and Method for Diagnosis  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: 119 No. 5741645th Fourth Street, Suite 203  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,802B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muetting, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110.00030101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1225  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-469-802B-29

Query Match 0.8%; Score 23; DB 1; Length 66;  
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTGTG 1568  
|||||  
DB 41 GTGTGTGTGTGTGTGTGTGTGTG 63

Search completed: June 28, 2003, 11:10:35  
Job time: 159 secs



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IMMEDIATE SOURCE:  
CLONE: mfd12rs  
US-08-222-177A-86

Query Match 0.8%; Score 23; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.48; 0; Indels 0;  
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568  
DB 36 GTGTGTGTGTGTGTGTGTGTG 14

22 nks

RESULT 11

US-08-222-177A-152/c  
Sequence 152, Application US/08222177A  
Patent No. 5582979

GENERAL INFORMATION:

APPLICANT: Weber, James L.  
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 460  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dewitt Ross & Stevens, S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53717-1914

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,177A  
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/341,562  
FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 09865.601  
TELEPHONE: (608) 831-2100  
TELEFAX: (608) 831-2106  
TELEX:

INFORMATION FOR SEQ ID NO: 152:

SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
IMMEDIATE SOURCE:  
CLONE: mfd34rs  
US-08-222-177A-152

Query Match 0.8%; Score 23; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568  
DB 24 GTGTGTGTGTGTGTGTGTGTG 2

RESULT 12

US-08-469-802B-27/c  
Sequence 27, Application US/08469802B  
Patent No. 5741645

GENERAL INFORMATION:

APPLICANT: Orr, Harry T.  
APPLICANT: Ranum, Laura P.W.  
APPLICANT: Chung, Ming-yi  
APPLICANT: Zoghbi, Huda Y.  
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia  
Patent No. 5741645  
TITLE OF INVENTION: Type 1 and Method for Diagnosis  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: 119 No. 5741645th Fourth Street, Suite 203  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,802B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muetting, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110.00030101  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1225

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:  
LENGTH: 54 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-469-802B-27

Query Match 0.8%; Score 23; DB 1; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1546 GTGTGTGTGTGTGTGTGTGTG 1568  
DB 47 GTGTGTGTGTGTGTGTGTGTG 25

RESULT 13

US-08-267-803B-45/c  
Sequence 45, Application US/08267803B  
Patent No. 5834183

GENERAL INFORMATION:

APPLICANT: Orr, Harry T.  
APPLICANT: Ranum, Laura P.W.  
APPLICANT: Chung, Ming-yi  
APPLICANT: Zoghbi, Huda Y.  
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia  
Patent No. 5834183

TITLE OF INVENTION: Type 1 and Method for Diagnosis  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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Creation date: 09-22-2004  
Indexing Officer: BHULUKA - BEKANA HULUKA  
Team: OIPEBackFileIndexing  
Dossier: 09670568

Legal Date: 07-07-2003

No.	Doccode	Number of pages
1	SRNT	4

Total number of pages: 4

Remarks:

Order of re-scan issued on .....

